November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

```
                 GenCore version 5.1.6
          Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:   January 10, 2006, 16:26:16 ; Search time 395 Seconds
                                        (without alignments)
                                        8446.793 Million cell updates/sec

Title:          US-09-367-052-1
Perfect score:  1877
Sequence:       1 ccatcctaatacgactcact.........aaaaaaaaaaaaaaaaa 1877

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:    2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents_NA:*
    1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
    2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
    3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
    4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
    5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
    6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
    7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
    8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
    9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	974.4	51.9	1737	2	US-08-202-056-4	Sequence 4, Appli
2	974.4	51.9	1737	2	US-08-076-093A-3	Sequence 3, Appli
3	974.4	51.9	1737	2	US-08-701-265-3	Sequence 3, Appli
4	974.4	51.9	1737	2	US-08-284-586-3	Sequence 3, Appli
5	974.4	51.9	1737	2	US-08-805-478-3	Sequence 3, Appli
6	974.4	51.9	1737	2	US-08-802-627A-3	Sequence 3, Appli
7	974.4	51.9	1737	2	US-08-801-238-3	Sequence 3, Appli
8	974.4	51.9	1737	2	US-08-801-228-3	Sequence 3, Appli
9	974.4	51.9	1737	3	US-09-104-296-3	Sequence 3, Appli
10	974.4	51.9	1737	6	PCT-US94-06380-2	Sequence 2, Appli
11	952.8	50.8	1679	3	US-09-517-605-14	Sequence 14, Appl
12	951.8	50.7	1664	3	US-09-582-224A-5	Sequence 5, Appli
13	951.8	50.7	1664	3	US-09-023-655-1213	Sequence 1213, Ap
14	859	45.8	1225	3	US-09-016-434-1235	Sequence 1235, Ap
15	834.6	44.5	1317	2	US-08-153-848-45	Sequence 45, Appl
16	834.6	44.5	1317	3	US-09-299-843A-45	Sequence 45, Appl
17	834.6	44.5	1317	3	US-09-088-337B-45	Sequence 45, Appl
18	834.6	44.5	1317	6	PCT-US93-11153-45	Sequence 45, Appl
19	809.6	43.1	1059	3	US-09-647-501-1	Sequence 1, Appli
20	804.8	42.9	1059	3	US-09-826-509-484	Sequence 484, App
21	282	15.0	440	3	US-09-513-999C-1915	Sequence 1915, Ap
22	198.4	10.6	1119	3	US-09-170-496D-65	Sequence 65, Appli
23	198.4	10.6	1679	2	US-08-202-056-6	Sequence 6, Appli
24	198.4	10.6	1679	2	US-08-076-093A-5	Sequence 5, Appli
25	198.4	10.6	1679	2	US-08-701-265-5	Sequence 5, Appli
26	198.4	10.6	1679	2	US-08-284-586-5	Sequence 5, Appli
27	198.4	10.6	1679	2	US-08-805-478-5	Sequence 5, Appli
28	198.4	10.6	1679	2	US-08-802-627A-5	Sequence 5, Appli
29	198.4	10.6	1679	2	US-08-801-238-5	Sequence 5, Appli
30	198.4	10.6	1679	2	US-08-801-228-5	Sequence 5, Appli
31	198.4	10.6	1679	3	US-09-104-296-5	Sequence 5, Appli
32	198.4	10.6	1679	6	PCT-US94-06380-3	Sequence 3, Appli
33	198.4	10.6	2802	3	US-09-949-016-4384	Sequence 4384, Ap
34	198.4	10.6	2818	3	US-08-982-493-7	Sequence 7, Appli
35	198.4	10.6	2818	3	US-08-628-655-1	Sequence 1, Appli
36	198.4	10.6	16404	3	US-09-949-016-16126	Sequence 16126, A
37	196.8	10.5	1119	3	US-09-170-496D-199	Sequence 199, App
38	195.8	10.4	2085	3	US-09-299-843A-65	Sequence 65, Appli
39	195.8	10.4	2085	3	US-09-088-337B-65	Sequence 65, Appli
40	193.8	10.3	1107	3	US-09-170-496D-19	Sequence 19, Appli
41	193.8	10.3	1293	3	US-09-016-434-1052	Sequence 1052, Ap
42	193.8	10.3	1670	3	US-08-709-838-1	Sequence 1, Appli
43	193.8	10.3	1670	3	US-08-829-839-1	Sequence 1, Appli
44	193.8	10.3	1670	3	US-09-023-655-980	Sequence 980, App
45	193.8	10.3	1670	3	US-09-624-594-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
US-08-202-056-4
; Sequence 4, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
;   APPLICANT: Chuntharapai, Anan
;   APPLICANT: Hebert, Caroline
;   APPLICANT: Kim, Kyung Jin
;   APPLICANT: Lee, James
;   TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 460 Point San Bruno Blvd
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: patin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/202,056
;   FILING DATE: 25-FEB-1994
;   CLASSIFICATION: 436
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/677211
;   FILING DATE: 29-MAR-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Love, Richard B.
;   REGISTRATION NUMBER: 34,659
;   REFERENCE/DOCKET NUMBER: 706P3
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415/225-5530
;   TELEFAX: 415/952-9881
;   TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1737 bases
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-08-202-056-4

Query Match    51.9%;  Score 974.4;  DB 2;  Length 1737;
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Best Local Similarity   76.1%;   Pred. No. 1.2e-181;
Matches 1391; Conservative   0; Mismatches 301; Indels 136; Gaps 10;

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Qy    50 GCAGGTAGCAGTGACCCTCTGAGCGTTTGGTGCTCCGGTAACCACCACGGCTGTAGAGC  109
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Qy   110 GAGTGTTGCCATGGAACCGATCAGTGTGAGTATAACACTTCTGATAACTACTCTGAGA  169
         |||||  ||||         ||| || || ||| | |||||||||||  |||||||
Db    80 CAGCGGTTACCATGGA-----GGGGATCAGTATATACACTTCAGATAACTACTCACCGAGGA  134

Qy   170 AGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCCGGGATGAAAAACGTCCA  229
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Db   135 AATGGGCTCAGGGGACTATGACTCCCATGAAGGAACCCTGTTTCCGTGAAGAAAAATGCTAA  194

Qy   230 TTTCAATAGGATCTTCCTGCCACCATCACTTCTTCATCATCTTCTTACACTGGCATAGTCGG  289
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Qy   350 GTACCGGCTGCACCTGTCAGTGGCTGCTGACCTCCTCTTGTCATCACACTCCCCTTCTGGGC  409
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Db   315 GTACAGGCTGCACCTGTCAGTGGCCGCCGACCTCCTCTTGTCATCACGCTTCCCTTCTGGGC  374

Qy   410 AGTTGATGCATGCCGTGGTACTTTGGAAATTTTGTGTAAGGCTGTCCATATCAT  469
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Qy   530 CCTCGCCATTGTCCACGCCACCACCAGTCAAAGGCCAAGCAAGGAGAAGCTGGCTGAAAAGGC  589
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Qy   590 AGTCTATGTGGGCGTCTGATCCCAGCCCTCCTCGACTATACCGACTTCATCTTTGC  649
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Qy   650 CGACGTCAGCCAGGGGGATGACAGTACATCTGTGACCGCCTTTA  709
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Qy   710 CCCCGATAGCCTGTGGATGGTGTCTTCAATTCAGACATATAATGAGTGGGTCATCCT  769
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Db   720 GCCTGGTATTGTCATCATCTCTGTGTGTGTGCTATTGCATTATCATCTTCAAGCTGTCACACTCCAA  779

Qy   830 GGGCCACCAGAAGCGCAAGGCCCTCAAGACGCACAGTCATCCTCAGCTTCTTCTTGC  889
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Db   780 GGGCCACCAGAAGCGCAAGGCCCTCAAGACCACCAGTCATCCTCCTGGCTTTCTTCGC  839

Qy   890 CTGCTGGCTGCCATATTATGTGGGGATCAGCATCAGCGACTTCCTCTTTTGGGAGTCAT  949
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Db   840 CTGTTGGCTGCCTTACTACATTGGGGATCAGCATCGACTTCCTCATCCTCTGTGAAATCAT  899

Qy   950 CAAGCAAGGATGTGACTTCGACAAGTGCACAAGTGATCCTCATCACAGAGGGCCCT  1009
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Db   900 CAAGCAAGGTGTCAGTTTGAGAACATTGTGCACAAGTGATTTCCATCACCGAGGGCCCT  959

Qy  1010 CGCCTTCTTCCACTGTTGCCTGACCCCATCCTCTGCCTTCCTCTATGCCTTCCTCGGGGCAAGTTCAA  1069
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Qy  1070 AAGCTCTGCCCAGCACTCAACTCCATGAGCGAGAGGCTCCAGCCTCAAGATCCTTTC  

Qy  1130 CAAAGGAAAGCGGGTGGGACACTCTTCCGTTCCGTCCCACGGAGTCAGGAGTCAGAATCCTCCAGTTTTCA  1189
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Db  1080 CAAAGGAAAGCGAGTGGGACCATTCATCGTGTTCCACTGAGTCTTCAAGTTCTTCAAGTTTTCA  1139

Qy  1190 CTCCAGTCAACCCTTATGCAAAGACTATTATATATAATATATATAGATGAAAATAACTTTT  1249
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Db  1140 CTCCAGCTAA-------CACAGATGTAAAAGACTTTTTTTTATACGATAAAATAACTTTTT  1191

Qy  1250 TTTTATGTTACACATTTCCAGATATAAGACTGACCAGTCTTGTACACAGTTTTTTTTTT  1309
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Db  1192 TTTTAAGTTACACATTTTCAGATATAAAAGACTGACCAATATGTACAGTTTTTTATTGC  1251

Qy  1310 TTTTTAATTGACTGCTGTGGGAGTTTATGTTCCCAGTTTTTGTGAGGTTGTTGACTTAATTT  1369
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Db  1252 TTGTTGGATTTTGT------CTTGTGTTTCTTTAGTTTTTGTGAAGTTTAATTGACTTA  1305

Qy  1370 ATATAAATATTGTTTTGTTGTTCATGTGAATGACCTGTGTGTAGGACTGTGAATGAGAAACTGA  1429
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Db  1306 TTTATA---TAAATTTTTTTTGTTTCATATTGATGTGTGTAGGACTGTAGAA------AAGGGACTGA  1361

Qy  1430 AAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTGTGGTAGAACTGTGAGAGGAAGAAACTGA  1489
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Db  1362 AAGTTCTTAGTTGCTGTATGTCTCGTGGGTAGGACTGTAGAA-------AAGGGACTGA  1413

Qy  1490 ACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTTGCTGCA  1549
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Db  1414 ACATTCCAGAGCGTGTAGTGAATCACGTAAAGCTAGAATGATCCCCAGCTGTTTATGCA  1473

Qy  1550 TAATCTCTTCATTCCGAGGAGCACCCCACCCCACCCCCATTCTTAAAT  1609
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Db  1474 TAGATAATCTCTCCA---------------------------------  1488

Qy  1610 TGTTTGGTTATGCTGTGTGATGGTTTTGTTGGTTTTTTTTTGTTGTTTGTTTTT  1669
                                           ||||||||||
Db  1489 ----------------------------------TTCCCGTGGAACGTTTTTCCTGTTCTTAAGACGTGAT  1525

Qy  1670 TTTTCGTAAAGATGGCACTTAAAACCAAAGCCTGAAATGGTCGTAGAAATGGTCGTGGGGT  1729
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Db  1526 TTTGCTGTAGAAGATGGCACTTATAACCAAAGCCCAAAGTGGT-ATAGAAATGCTGG---  1581

Qy  1730 TTTTTTGTTGTTGTTGTTTTTTCAGTTTTTTCAGTTTTGACTTCAGTCCCTACAAAT  1789
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Db  1582 -------------------------TTTTTCAGTTTTTCAGGAGTGGGTTGATTTCAGCCACCTAC-AGT  1623

Qy  1790 GTACAGTCTTGTATTACATTGTTAATAAAGTCAATGGATAAAACTTAAAAAAAAAAA  1849
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Db  1624 GTACAGTCTTGTATTAAGTTGTTAATAAAGTACATGTTAAACTTAAAAAAAAAAAAAAAA  1683

Qy  1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  1877
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Db  1684 AAAAAAAAAAAAAAAAAAAAAAAAAAAA  1711
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COMPUTER READABLE FORM:
    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/076,093A
    FILING DATE: 11-Jun-1993
    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 07/810782
    FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 07/677211
    FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
    NAME: Love, Richard B
    REGISTRATION NUMBER: 34,659
    REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415/225-5530
    TELEFAX: 415/952-9881
    TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
        LENGTH: 1737 nucleotides
        TYPE: Nucleic Acid
        STRANDEDNESS: Single
        TOPOLOGY: Linear

US-08-076-093A-3

Query Match       51.9%;   Score 974.4;  DB 2;  Length 1737;
Best Local Similarity 76.1%;  Pred. No. 1.2e-181;
Matches 1391;  Conservative 0;  Mismatches 301;  Indels 136;  Gaps 10;
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Db    80 CAGGGGTTACCATGA------GGGGATCAGTATATACACTTCAGATAACTACACCGAGGA 134

Qy   170 AGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGATGAAAACGTCCA 229
              ||| ||| | ||||| |||||||||| || ||||||||| |||  |||||| | |
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Qy   230 TTTCAATAGGATCTTCCTGCCCACCATCCATCATCTTCTGACTGGCGATAGTCGG 289
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Db   195 TTTCAATAAAATCTTCCTGCCCACCATCCATCATCTTCTTAACTGGCATTGTGGG 254

Qy   290 CAATGGATTGGTGATCCTGTCATGGGTTACCAGAGAGAACTAAGGAGCATGACGGACAA 349
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Db   255 CAATGGATTGGTCATCCTGTCATGGGTTACCAGAGAAGAAACTGAGAAGCATGACGGACAA 314

Qy   350 GTACCGGCTGCACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGGGC 409
          ||||   ||||||||||||||||| ||||||||||||||||||||| || ||||||||||
Db   315 GTACAGCGCTGCACCTGTCAGTGGCCGACCTCCTCTTTGTCATCACGCTTCCCCTTCTGGGC 374

Qy   410 AGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAGGCGTCCATATCAT 469
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Db   375 AGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCAT 434

Qy   470 CTACACTGTCAACCTCCTACAGCAGGTTCTCATCCTGGCCTTCATCAGCCTGACCGGTA 529
          ||||  ||||||||||||||||||| | ||||||||||||||||||| ||||||  |||
Db   435 CTACCAGTCAACCTCCTACAGCAGTGTCCTCATCCTGGCCTTCATCAGTCTGACCGCCTA 494

Qy   530 CCTCGCCATTGTCCACGCCACCAACAGTCAAAGGCCAAGGAGAAACTGCTGCTGAAAAGGC 589
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Db   495 CCTGCCCATCGTCCACGCCACCAACAGTCAGAGGCCAAGGAGAAGCTGTTGCGTGAAAAGGT 554

Qy   590 AGTCTATGTGGGGCTCTGGATCGATCCCCTGCTGCGACTATACCTGACTTCATCTTTGC 649
           |||||||| |||||  |         |||||||||||||| ||   |||||||||||
Db   555 GGTCTATGTTGGGCTGCTC-------CTCCTGCTGCGATATTCCGACTATTCCATCTTTGC 614

Qy   650 CGAGTCAGCCAGGGGACATCAGTCAGGGGATGACAGTACATCGTGACGGCCTTTA 709
           ||||                |||||||| |||||||| |||| ||||| ||| |
Db   615 CAACG-------TCAGTGAGGCAGATGACAGATAATCGTGACCGGCTTCTA 659

Qy   710 CCCCGATAGCCTGTGGATGGTGGTGTTCAATTCCAGCATATAATGGTGGGTCTCATCCT 769
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Db   660 CCCCAATGACTTTGGGTGGGTGGTTCAGTTTCAGCACATCATGGGTTCGCCTTATCCT 719

Qy   770 GCCCGGCATGCATCATCCTCCTGTACTGCATCATCATATTCATTCATCTCCAAGCTGTCCCAA 829
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Db   720 GCCTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATCTCCAAGCTGTCCCAA 779

Qy   830 GGGCCACCAGAAGCCCAAGACGCCTCAAGACAGCAGTCATCCTCATCCTCAGCAGTCTTCTTGC 889
          |||||||||||||||||||||||||||||| |||| ||||| ||||||| |||| | |||| ||
Db   780 GGGCCACCAGAAGCCCAAGACGCCTCAAGACCAGCCACAGTCATCGTCATCCTCTTCTTCGC 839

Qy   890 CTGCTGGCTGCCATTATGTGGGGATCACAGCATCAGCACTCCTTTTTGGGAGTCAT 949
          || ||||||||| ||| ||||||||||||||| ||||||||| |||| ||| ||||
Db   840 CTGTTGGCTGCCCTTACTACATATGGGGATCAGCACTCCACTCCTCTGGAAATCAT 899

Qy   950 CAAGCAAGGATCGTGACTTGCACAAGTGACTCCATCCTCCATCACAGAGCGCCCT 1009
          || | |||| |||||| | ||| |||| ||| ||||||||| || |||| ||||
Db   900 CAACAAGGTGTGACTGAGTTTGAGAACACCGTGCACAAGTGGATTTCCATCACCGAGGCCCT 959

Qy  1010 CGCCTTCTTCCACTGTTGCCTCAACCCATCCTCCCGGGCCAAGTTCAA 1069
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Db   960 AGCTTTCTTCCACTGTTGTCTCAACCCCATCCTCCTGTTCCTGGAGCCAAATTTAA 1019

Qy  1070 AAGCTCTGCCCAGCACTCAACTCATGAGCAGAGGCTCCAGCCTCAAGATCCTTTC 1129
          ||  |||||||||| ||||| || |||||||||| |||||||||||||||| |||
Db  1020 AACCTCTGCCCAGCCAGCACTCACCTCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTC 1079

Qy  1130 CAAAGGAAAGCGGGGTGGCAACTCTTCCGTCTCCGGAGTCTTCCAGTTTCA 1189
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Db  1080 CAAAGGAAAGCGGAGTGGACATTCATCGTGTTCCACTGAGTCTTCAAGTTTTCA 1139

Qy  1190 CTCCAGTCAACCCTTATGCAAAGACTTATTATAATTATATATATATGATAAAGAACTT 1249
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Qy  1730 TTTTTTGTTTGTTTGTTTTTTCAGTTTTCAAGAGTAGATTGACTTCAGTCCCTACAAAT 1789
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Db  1582 --------------TTTTTCAGTTTTTCAGGAGTGGGTTGATTTCAGCACCTAC-AGT 1623

Qy  1790 GTACAGTGTCGTATTACATTGTTAATAAAGTCAATGATAAACTTAAAAAAAAAAAAAA 1849
          |||||||  ||||||| | ||||||||||| |||| ||||||||||||||||||||||
Db  1624 GTACAGTCCTGTATTAAGTGTTAATAAAGTACATGTTAAACTTAAAAAAAAAAAAAAA 1683

Qy  1850 AAAAAAAAAAAAAAAAAAAAA 1877
          |||||||||||||||||||||
Db  1684 AAAAAAAAAAAAAAAAAAAAA 1711
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RESULT 3
US-08-701-265-3

; Sequence 3, Application US/08701265
; Patent No. 5776457
GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 460 Point San Bruno Blvd
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/701,265
;   FILING DATE: 22-AUG-1996
;   CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/076093
;   FILING DATE: 11-Jun-1993
;   APPLICATION NUMBER: 07/810782
;   FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/677211
;   FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Love, Richard B
;   REGISTRATION NUMBER: 34,659
;   REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415/225-5530
;   TELEFAX: 415/952-9881
;   TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1737 nucleotides
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
US-08-701-265-3

Query Match   51.9%; Score 974.4; DB 2; Length 1737;
Best Local Similarity 76.1%; Pred. No. 1.2e-181;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

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Qy    50 GCAGGTAGCAGTGACCCCTCTGAGGCGTTTGGTGCTCCGGTAACCACCACGGCTGTAGAGC 109
          || |  |||| ||||| | ||||| |||  ||||||| || |||||| |||| || ||| |
Db    20 GCGCGGGCGCAAAGTGACGCCGAGGGCCTCCAGTGCTCCAGTAGCCACCGACCATCTGGAGAAC 79
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          |||||||||          ||||| ||     |    | |     |  | ||||
Db   1140 CTCCAGCTAA-------CACAGATGTAAAAGACTTTTTTTATACGATAAATAACTTTT 1191

Qy   1250 TTTTATGTTACACATTTCCAGATATAAGAGACTGACCAGTCTTGTACAGTTTTTTTTTT 1309
          |||||||||||||||||||||||   ||||| ||||||||||||||||||  ||||||
Db   1192 TTTTAAGTTACACATTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTTTTATTGC 1251

Qy   1310 TTTTTAATTGACTGTTGGGAGTTTATGTTCCTCGAGTTTTTGTGAGGTTTGACTTAATTT 1369
          ||  ||       ||||| ||  ||||||||||||||||
Db   1252 TTGTTGGATTTTGT-------CTTGTGTTTCTTTAGTTTTTGTGAAGTTTAATTGACTTA 1305

Qy   1370 ATATAAATATTGTTTTTTGTTGTTCATGTGAATGAGCGTCTAGGCAGGACCTGTGGCC 1429
          ||||  ||      ||||||||||||||||||||||||||| ||||||||||||||
Db   1306 TTTATA----TAAATTTTTTTGTTTCATATTGATGTGTGTCTAGGCAGGACCTGTGGCC 1361

Qy   1430 AAGTTCTTAGTAGCTGTCTTATCTGTGTGTAGGACTGTAGAACTGTAGAGGAAGAAACTGA 1489
          ||||||||||||| ||||||||||||||||||           ||||||||||||
Db   1362 AAGTTCTTAGTTGCGTATGTCTCTCGTGGTAGGACTGTAGAA-------AAGGGAACTGA 1413

Qy   1490 ACATTCCAGAAATGTGTGGTAAATTGAATAAAGCTAGCCGTAGTCCTCAGCTGTTGCTGCA 1549
          |||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db   1414 ACATTCCAGAGGCGTGAGTCAGTAGTGAATCACGTAAAGCTAGAAATGATCCCCAGCTGTTTATGCA 1473

Qy   1550 TAATCTCTTCATTCCGAGGAGCACCCCACCCCCACCCCCATTCTTAAAT 1609
          || |            |  |
Db   1474 TAGATAATCCTCCA-------TAGATAATCTCTCCA- 1488

Qy   1610 TGTTTGGTTATGCTGTGTGATGGTTGTTTGGTTTTGTTTTTGTTGTGTTTT 1669
          |||||||||||||||||||||||||||||||
Db   1489 ------------------TTCCCGTGGAACGTTTTTCCTGTTCTTAAGACGTGAT 1525

Qy   1670 TTTTCTGTAAAAGATGGCACTTAAAACCTAAAAGCCTGAAATGGTGTAGAAATGTGGGGT 1729
          |||  |       ||||||| ||||||||||||||||  ||||||||||||
Db   1526 TTTGCTGTAGAAGATGGCACTTATAACCAAAGCCCAAAGTGGT-ATAGAAATGCCTGG--- 1581

Qy   1730 TTTTTTTTGTTTGTTGTTTTTTCAGTTTTTCAAGAGTAGATTGACTTCAGTCCCTACAAAT 1789
          ||||||||||||||||||||||||||||||
Db   1582 -------------TTTTTCAGTTTTTCAGGAGTGGGTTGATTTCAGCCACCTAC-AGT 1623

Qy   1790 GTACAGTCTTGTATTACATTGTAATAAAGTCAATGATAAACTTAAAAAAAAAAAAAAA 1849
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1624 GTACAGTCTTGTATTAAGTTGTTAATAAAAGTACATGTTAAAACTTAAAAAAAAAAAAAA 1683

Qy   1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
          ||||||||||||||||||||||||
Db   1684 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1711
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RESULT 4
US-08-284-586-3
; Sequence 3, Application US/08284586
; Patent No. 5840856
GENERAL INFORMATION:
   APPLICANT: Chuntharapai, Anan
   APPLICANT: Lee, James
   APPLICANT: Hebert, Caroline
   APPLICANT: Jin Kim, K.
   TITLE OF INVENTION: Antibodies to Human PF4A Receptors
   NUMBER OF SEQUENCES: 6
   CORRESPONDENCE ADDRESS:
      ADDRESSEE: Genentech, Inc.
      STREET: 460 Point San Bruno Blvd
      CITY: South San Francisco
      STATE: California
      COUNTRY: USA
      ZIP: 94080
   COMPUTER READABLE FORM:
      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: WinPatin (Genentech)
   CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/284,586
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      FILING DATE:
      CLASSIFICATION: 424
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US/08/076,093A
      FILING DATE:    11-Jun-1993
      APPLICATION NUMBER: 07/810782
      FILING DATE:    19-DEC-1991
   PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 07/677211
      FILING DATE:    29-MAR-1991
   ATTORNEY/AGENT INFORMATION:
      NAME: Love, Richard B
      REGISTRATION NUMBER: 34,659
      REFERENCE/DOCKET NUMBER: 706P2
   TELECOMMUNICATION INFORMATION:
      TELEPHONE: 415/225-5530
      TELEFAX: 415/952-9881
      TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:  3:
   SEQUENCE CHARACTERISTICS:
      LENGTH: 1737 nucleotides
      TYPE: Nucleic Acid
      STRANDEDNESS: Single
      TOPOLOGY: Linear
US-08-284-586-3
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Query Match         51.9%;   Score 974.4;   DB 2;   Length 1737;
Best Local Similarity  76.1%;   Pred. No. 1.2e-181;
Matches 1391;   Conservative  0;   Mismatches  301;   Indels 136;   Gaps 10;

Qy    50 GCAGGTAGCAGTGACCCTCTGAGGCGTTGTGTCCGGTAACCACCACCGGCTGTAGAGC 109
          ||| |||||    |||||||||||||   ||||||||||||||||||||||||
Db    20 GCGCGGCGCAAAGTGACGCCGAGGGCCTGCCGAGTGCTCAGTGCGTCCACCGCATCTGGAGAAC 79

Qy   110 GAGTGTTGCCATGGAACCGATCAGTGTGAGTAGTATATACACTTCTGATAACTACTCTGAAGA 169
          |||||||||        ||||||||||||||||||||||||||||||
Db    80 CAGGGATCAGTATATACACTTCAGATAACTACACCGAGGA 134

Qy   170 AGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAAGCTCCA 229
          ||||||||||        ||||||||||||||||||||||||||||
Db   135 AATGGGCTCAGGGGACTATGACTCCATGGAACGAACCCTGTTTCCGTGAAGAAAATGCTAA 194

Qy   230 TTTCAATAGGATCTTCCTGCCACCATCTACTTCAATTCGGTCATCATGCATGCTGGCATAGTCGG 289
          |||||||||     ||||||||||||||||||||||||||||   ||||||||||
Db   195 TTTCAATAAAATCTTCCTGCCACCATCTACCTACTTCTTCTAACTGGCATTGTGGG 254

Qy   290 CAATGGATTGGTGATCCTGTGTCATGGGTCATGGGTTACCAGGAGAGAAGTAAGGAGAAACTGAGAGAACAA 349
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   255 CAATGGATTGGTCATCCTGGTCATGGGTTACCAGGAGAGAAGTAAGGAGAAACTGAGAGAACAA 314

Qy   350 GTACCGGCTGCACCTGTCAGTGGCTGACCTCCTTGTCATCAACACTCCCCTTCTGGGC 409
          |||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db   315 GTACAGGCTGCACCTGTCAGTGGCTCAGTGCTCAGTGCTCCACCGCTTCCTTCGTGGGC 374

Qy   410 AGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAGGCTGTCCATATCAT 469
          |||||||||||||||||||||||| ||||||||||||||||||||||
Db   375 AGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCTGGGAAGCAGGCAGTTCCATGTCAT 434

Qy   470 CTACACTGTCAACCTTCTACAGCAGGTTCATCCTGGCCTTCATCAGCCTGGACCGGTA 529
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   435 CTACACAGTCAACCTCTACAGCAGTGTCCTCATCCTGGCCTTCATCAGCCTGGACCGCTA 494

Qy   530 CCTCGCCATTGTCCACGCCACCAACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGC 589
          |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db   495 CCTGGCCATCGTCCACGCCACCAACAGTCAGAGGCCAAGGAAACTGCTGGCTGAAAAAGGT 554

Qy   590 AGTCTATGTGGGGGTCTGGATCCCTGCCCTCCTGCTCGACTATACCTGACTTCATCTTTGC 649
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   555 GGTCTATGTGGCGTCTGGATCCCTGCCCTGCTCGACTATTCCCGACTTCATCTTTGC 614

Qy   650 CGACGTCAGCCAGGGGGACACTCAGTCAGGGATGACAGTGACAGTTACAGTATGTCTGTGACCGCTTTA 709
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Db   615 CAACG-------TCAGTGAGGCAGCAGATGACAGAGATATACTCGTGACCGCTTCTA 659
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Qy  1790 GTACAGTCTTGTATTACATTGTTAATAAAGTCAATGATAAACTTAAAAAAAAAAAAAAAA 1849
         ||||||||||||||||||| |||||| ||||||| |||||||||||||||||||||||||
Db  1624 GTACAGTCTTGTATTAAGTTGTTAATAAAGTGTTAAACTTAAAAAAAAAAAAAAAAAAAA 1683

Qy  1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
         ||||||||||||||||||||||||||||
Db  1684 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1711
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RESULT 5
US-08-805-478-3
; Sequence 3, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
;; APPLICANT: Chuntharapai, Anan
;; APPLICANT: Lee, James
;; APPLICANT: Hebert, Caroline
;; APPLICANT: Jin Kin, K.
;; TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 460 Point San Bruno Blvd
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatin (Genentech)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/805,478
;; FILING DATE: 25-Feb-1997
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/284586
;; FILING DATE: 10-AUG-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/076093
;; FILING DATE: 11-JUN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/810782
;; FILING DATE: 19-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P0706P2P1C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-5530
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1737 base pairs
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Single
;; TOPOLOGY: Linear
US-08-805-478-3

Query Match   51.9%; Score 974.4; DB 2; Length 1737;
Best Local Similarity   76.1%; Pred. No. 1.2e-181;
Matches 1391; Conservative   0; Mismatches 301; Indels 136; Gaps 10;

Qy   50 GCAGGTAGCAGTGACCCCTGAGGCGGTTGGTGCTCCGGTAACCACCACGCTGTAGAGC 109
         |||||| ||| |||| ||||| ||||||| || |||||| |||| || |||
Db   20 GCGCGGCGCAAAGTGACGGCCGAGGGGCCTGAGTGCTTCCAGTAGCCACCATCTGGGAGAAC 79

Qy   110 GAGTGTGCCATGAACCGATCAGTGTGAGTATATACACTTCTGAGTATCTGAAGA 169
         || |||||| || || || |||||| |||||| ||||| ||||
Db   80 CAGCCGGTTACCATGA-----GGGGATCAGTATATACACTTCAGATAACTACACACCCGAGGA 134
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Qy   710 CCCCGATAGCCTGTGGATGTGTGTTTCAATTCCAGCATATAATGTGGGTCTTCATCCT 769
         |||| |||||  |||||||||| |||||| |||||||| |  | |||| ||||| |||
Db   660 CCCCAATGACTTGTGGGGTGGTTGTGTTCCAGTTTCAGTTTCAGCACATCATGGTTGGCCCTTATCCT 719

Qy   770 GCCCGGCATCGTCATCCTCTTCTGTACTGACTCATCATCATCTCTAAGCTGTCACACTCCAA 829
         || |||||||| ||||| ||||| |  || |  |  ||| |||  |  ||||||||||||||
Db   720 GCCTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATTCTTCCAAGCTGTCACACTCCAA 779

Qy   830 GGGCCACCAGAAGGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTTCTTCTTGC 889
         |||||||||||||||||||||||||  ||| ||| |||  |  || |||| ||| |||
Db   780 GGGCCACCAGAAGCGCAAGGCCCTCAAGACCACCACCAGTCATCCTCTGGCTTTCTTCGC 839

Qy   890 CTGCTGGCTGCCATATATGTGGGGATCAGCATCGACTCCTTTGGGAGTCAT 949
         |||| |||| | |||  | |||| ||  |  ||  ||| || |  ||||||
Db   840 CTGTTGGCTGCCTTACTACATCAGCAGCATCAGCATCTCCTTGTCCTGGAAATCAT 899

Qy   950 CAAGCAAGGATGTGACTTCGAGAGCAGCATTGTGCACAAGTGGATCTCCATCACACGAGGCCCT 1009
         |||||||||||||| ||| || ||| ||||| |  |||| |||| ||||| |||| |||||||
Db   900 CAAGCAAGGGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCCATCACCACGAGGGCCCT 959

Qy  1010 CGGCTTCTTCCACTGTTGCCTGAACCCCATCCTCTATGCCTTCCTCGGGGCCAAGTTCAA 1069
         | |||||||||||| ||| |||||||||||||  || |  |||| ||| |||||   ||
Db   960 AGTTCTTCCACTGTTGCTGAACCCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAA 1019

Qy  1070 AAGCTCTGCCCAGCATGACACTCAACTCCATTGAGCAGAGGCTCCAGCCTCCAAGATCCTTTC 1129
         |||| || ||||| |||||| | |  ||| || |||||| |||||||| |||||| ||| |||
Db  1020 AACCTCTGCCCAGCATGACACGCTCACCTGTGAGCAGAGTGTCCAGCCTCCAAGATCCTCTC 1079

Qy  1130 CAAAGGAAAGCGGGGTGGACACTCTTCCGTCCGCGAGTCAGAATCCTCCAGTTTCA 1189
         ||||||||||| ||| | ||||| |||| || ||| |||||| ||||| ||| | |
Db  1080 CAAAGGAAAGCAGGTGAGGTGGACATTCATCTGTTCCACTGAGTCTTCAAGTTTCA 1139

Qy  1190 CTCCAGCTAACCCCTATGCAAAGACTTATATATATATATATGAATAAAGAAACTT 1249
         ||||||||    ||  ||| |||  | |||| |||| |  | |  || |  ||||
Db  1140 CTCCAGCTAA-------CACAGATGTAAAAGACTTTTTTTTTATACGATAAATAACTTTT 1191

Qy  1250 TTTTATGTTACACATTTTCCAGATATAGAGACTGACCAGTCTGTACAGTTTTTTTTTT 1309
         ||| | |||||||| |   |||| |||| ||||  ||||| |||||  |||||||||||
Db  1192 TTTAAGTTACACATTTT-CAGATATAAAAGACTGACCAATATTGTACAGTTTTTTATTGC 1251

Qy  1310 TTTTTAATTGACTGTGGAGGAGTTTATGTTCCTCTAGTTTTGTGAGGTTTGACTTAATTT 1369
         ||||  || | | ||| |||  ||  ||| || ||||||||||| || ||  ||| ||||
Db  1252 TTGTTGGATTTTTGT-------CTTGTGTTTCTTTAGTTTTGTGAAGTTTAATTGACTTA 1305

Qy  1370 ATATAAATATTGTTTTTTTGTTCATGTGAATGAGCGTCTAGGCAGGACCTGTGGCC 1429
         |  || |  | |||  |||| || ||| ||| ||||| |||||||||||||||||||
Db  1306 TTTATA-----TAAATTTTTTGTTTTTTGTTTCATATTGATGTGTGTCTAGGCAGGACCTGTGGCC 1361

Qy  1430 AAGTTCTTAGTAGCTGTTTATCTGTGTGGGACTGTAGAACTGTAGAGGAGAAACTGA 1489
         ||||| ||| | ||| | || || || ||| ||||| |    ||  ||||||||  |
Db  1362 AAGTTCTTAGTATGCTGTGTATGTCTCGTGGGACTGTAGAA------AAGGGAACTGA 1413

Qy  1490 ACATTCCAGAATGCATGGTGTGTAAATTGAATAAAGTCCTGATCTGTTGCTGCA 1549
         ||||| | | |  |  | | ||||   |  |   ||| || || ||||| ||||
Db  1414 ACATTCCAGAGCGTGTAGTGAATCACGTAAAGCTAGAAATGATCCCCAGCTGTTTATGCA 1473

Qy  1550 TAATTCTTCATTCCGAGGAGCACCCACCCCCACCCCCATTCTTAAAT 1609
         |   | | ||  | |  |  | |    |     ||||| ||||  |
Db  1474 TAGATAATCTCTCCA------------------------------- 1488

Qy  1610 TGTTTGGTTATGCTGTGTGTGATGGTTTGTTTGGTTTGTTTGTTGTTTGTTTTTT 1669
         ||||       |||   |||||| |||||||||||||||||| ||| || ||||||
Db  1489 -------------------TTCCCGTGGAACGTTTTTCCTGTTCTTAAGACGTGAT 1525

Qy  1670 TTTTCTGTAAAAGATGGCACTTAAAACCAAAGCCTGAAATGGTGTAGAAATGCTGGGGT 1729
         ||||| ||  | |  | |  | |||  ||||| ||| |   | ||| |||| | |   |
Db  1526 TTTGCTGTAGAGATGGCACTTATAACCAAAGCCCAAAGTGGT-ATAGAAATGCTGG--- 1581

Qy  1730 TTTTTTGTTTGTTTGTTTTTTTTTTTCAGTTTTTTTTCAGTTTTTTTTCAGTCCCTACAAAT 1789
         ||||  |          ||||| |||||||| |    ||||| |||| |||||| ||| |||
Db  1582 -------------TTTTTCAGTTTTTCAGGAGTGGTTGATTTGATTTCAGCACACTTAC-AGT 1623
```

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Qy   170 AGTGGGGTCTGGAGACTATGACTCCAACAGGAACCCTGCTTCCGGGATGAAAACGTCCA 229
         ||| |||||||||||||||||||||||  |  ||||||| | |||||||||| ||| ||
Db   135 AATGGGCTCAGGGGACTATGACTCCATGGAGGAACCCTGTTGTTCCGTGAAGAAAATGCTAA 194

Qy   230 TTTCAATAGGATCTTCCTGCCCACCATCATCTTCATCATCTTCTTCATCGACTGGCATAGTCGG 289
         |||||||  ||||||||||||||||||||||||||||||||||||| | ||||| ||| |||
Db   195 TTTCAATAAAATCTTCCTGCCCACCATCATCTTCATCATCTTCTTAACTGGCATTGTGGG 254

Qy   290 CAATGGATTGGTGATCCTGGTCATGGGTTACCAGAAGAAGCTAAGGAGCATGACGGACAA 349
         |||| |||||||||||||||||||||||||||| |||||||||||| |||||| ||||||
Db   255 CAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAAACTGAGAAGCATGACGGACAA 314

Qy   350 GTACCGGCTGCACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGGGC 409
         ||||||||||||||||||||||| ||||||||||||||| |||||||||||| |||||||
Db   315 GTACAGGCTGCACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGGGC 374

Qy   410 AGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAGGCTGTCCATATCAT 469
         |||| ||||| ||||||||| ||||| |||||||| ||||||| |||||||||||| |||
Db   375 AGTTGATGCCGTGGCTGGGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCAT 434

Qy   470 CTACACTGTCAACCTCTACAGCAGCGTTCTCATCCTGGCCTTCATCAGCCTGGACCGGTA 529
         |||| ||||||||||||||| |||||||||||||||||||||||||||| ||| |||  |
Db   435 CTACACAGTCAACCTCTACAGCAGCGTTCTCATCCTGGCCTTCATCAGCCTGGACCGGCTA 494

Qy   530 CCTGCCCATTGTCACGCCACCACCACCACAGTCAAAGGCCAAGGAAACTGTTGGCTGAAAAGGC 589
         |||||| ||||| |||||||||||||||||||||||||||||||| ||| |||||||||||
Db   495 CCTGGCCATCGTCACGCCACCACCACCACAGTCAAAGGCCAAGGAAACTGTTGGCTGAAAGGT 554

Qy   590 AGTCTATGTGGGGGTCTGGATCCCAGCCCTCCTGCTGACCATACCTGACTTCATCTTTGC 649
         |||| |||||||||||||||||||| |||||||| || ||||||  |||||||||||||||
Db   555 GGTCTATGTGGGGCTCTGGATCCCTGCTATTCCCGACTATACCAAGCCCGACTTCATCTTTGC 614

Qy   650 CGACTCAGCCAGGGGACATCAGTGCAGGGGATGACAGTACATCTGTGACCGCCTTTA 709
         |||  ||||||||   |||||||| | ||| ||||| ||  ||||| |||| |||||
Db   615 CAACG--------TCAGTGAGGCAGATGACAGATATCTGTGACCGGCTTCTA 659

Qy   710 CCCGATAGCCTGTGGATGGTGTTTCAATTGCTATTGCAATCATGTGGGTCTGGTCTCATCCT 769
         |||| ||||||| ||||| ||| |||||||| |||| |||||| ||| |||||||||||||
Db   660 CCCAATGACTTGTGTGGGTGGGTTGTTTCAGTTTCAGTTTCCTGCTATTATCCTCTATCCT 719

Qy   770 GCCCGGCATCGTCATCCTCTCCTGTACTACTGCAATCATGATCAGTACAGACACGTTCTTTTGC 829
         ||||||||||||||||||||||||| | ||||||||||| |||||| |||||||| |||| |||
Db   720 GCCTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCCAA 779

Qy   830 GGGCACCAGGAAGCCAAGGCCCTCAAGACGCACAGTCATCCTCTAGCTTCTTTTGC 889
         |||||||||||||||||||||||||||||| ||||||| || ||| |||||||||
Db   780 GGGCCACCAGGAAGCCAAGGCCCTCAAGACGCATCTCATCCTCATCCTCGGCTTTTCGC 839

Qy   890 CTGCTGGCTGCCATATTATGTGGGGATCCAGCATCGACTCCTTTTGGGAGTGTCAT 949
         |||| |||||| ||||| | |||||||||||||| ||||||||| |||||||| ||
Db   840 CTGTTGGCTGCCTTACTACATTGGGGATCAAGCACTGTTTCTCTGGAAATCATCAT 899

Qy   950 CAAGGAAGATGTGACTTCGAGAGTGTGCAACAGGTGACGTCCATCACAGAGGCCCT 1009
         ||||||||  ||| |||  |||| | ||| ||||||||||||||| |||||||||||
Db   900 CAAGGAGAAGCGAGGTGTGAGTTTGAGGACACTGTGCCACAAGTGGATTCCATCACCGAGGCCCT 959

Qy  1010 CGCCTTCTTCCACTGTTGCCTGAACCCCTTCATCTACGCTTCCTCGGGGCCAAGTTCAA 1069
         || ||||||||||||||| |||||||||||| | ||| ||||||||  ||||||| |||
Db   960 AGCTTTCTTCCACTGTTGTCTGAACCCCCTGCTTTACGTTTTCGTTGGAGCCAAATTTAA 1019

Qy  1070 AAGCTCTGCCCAGCATGCAACTCCAACTCCATGAGCAGCAGGCTCCAGGCCTCAAGATCCTTTC 1129
         ||||| |||| ||| | | ||||||| ||||||||||| ||||| ||||||||||| ||||||
Db  1020 AACCTCGCCAGCGCACTCACCTGTGAGCAGCAGAGGGTCCAGCCCCTCAAGATCCTCTC 1079

Qy  1130 CAAAGGAAAGCGCGGGTGGACACTCTTCCGTCCCACGAGTCAGAAAGTTCCAGTTTTCA 1189
         | |||||||||||| ||| ||||||||| ||| |||||||||||||||||||||||||||
Db  1080 CAAAGGAAAGCGAGGTGGACACTGTGCCACTGTGTTCCACTGAGTCTGAGTCTTCAAGTTTCA 1139

Qy  1190 CTCCAGCTAACCCTTATGCAAAGACTTATATATTTTTTTTTTTTATACGATAAAGAACTT 1249
         ||||| ||||     ||| |||| ||||||||||||||||||||||||||||||| |||||
Db  1140 CTCCAGCTAA------CACAGATGTAAAAGAACTTTTTTTTTATACGATGATAAATAACTTTT 1191

Qy  1250 TTTATGTTACACATTTTCCAGATATAAGAGACTGACCAGTCTTGTACAGTTTTTTTTTT 1309
         | |||||||||||||||| |||||||||||||| ||||  ||||| |||||||||||| ||
Db  1192 TTTAAGTTACACATTTTCAGATATAAAAAGACTGACCAATATTGTACAGTTTTTTTATTGC 1251

Qy  1310 TTTTTAATTGACTGTGTGGGAGGTTTATGTTCCTCTAGTTTTTGTGAGGTTTTGACTTAATTT 1369
         |||||| |||||| |||||||  | ||| |||||||||||||||||||| |||||||| |||
Db  1252 TTGTTGGATTTTGT-----CTTGTGTTTTCTTTAGTTTTTGTGAAGTTTAATTGACTTA 1305

Qy  1370 ATATAAATATGTTTTTGTTTGTTCATGTGAATGAGCGTCTAGGCAGGACCCTGTGGCC 1429
         |||||| ||||||||||  |||||| ||||||||||||||||||| ||| ||||||||
Db  1306 TTTATA---TAAATTTTTTTGTGTTTCATATTGATGTGTCTAGGCAGGACCCTGTGGCC 1361

Qy  1430 AAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTAGAGGAGAAAACTGA 1489
         ||||||||||||||||||||||||||| |||||| |||||||||
Db  1362 AAGTTCTTAGTTGCTGCTGTATGTCTCGTGGTAGGACTGTAGA--------AAGGGAACTGA 1413

Qy  1490 ACATTCCAGAATGTGTGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTTGTCTGCA 1549
         |||||||||||  ||| |||| ||||  |||||||||| ||| | ||| ||| ||||| ||
Db  1414 ACATTCCAGACGCGTGTAGTGAATCACGTAAAGCTAGAAAATGATCCCCAGCTGTTTATGCA 1473

Qy  1550 TAATCTCTTCATTCCGAGGAGCACACCCCCCACCCCCACCCCACCCCATTCTTAAAT 1609
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Db  1474 TAGATAATCTCTCCA--------------------------------------------- 1488

Qy  1610 TGTTTGGTTATGCTGTGTGATGGTTGTTTGTTTTTTTGTGTTGTGTTTTT 1669
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Db  1489 ----------------------TTCCCGTGGAAGGTTTTTTCCTGTTCTTAAGACGTGAT 1525

Qy  1670 TTTTCTGTAAAAGATGGCACTTAAAACCAAAGCCTGAAATGGTGGTGTAGAAATGCTGGGGT 1729
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Db  1526 TTTGCTGTGTAGAGATGGCACTATAACCAAAGCCCAAAGTGGT-ATAGAAATGCTG---- 1581

Qy  1730 TTTTTTGTTTGTTTGTTTGTTTCAGTTTCAAGAGTAGATTGACTTCAGTCCCTACAAAT 1789
         ||||||| | |||||||||||||||||||| |||||| ||| ||| |||||||||||
Db  1582 ---------------------TTTTTCAGTTTTCAGGAGTGGGTGATTTCAGCACCTAC-AGT 1623

Qy  1790 GTACAGTCTTGTATTACATTGTTAATAAACTTAAAAAAAAAAA 1849
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Db  1624 GTACAGTCTTGTATTAAGTTGTTAATAAAAGTACATGTTAAAACTAAAAAAAAAAAAAAA 1683

Qy  1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
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      APPLICATION NUMBER:  08/076093
      FILING DATE:  11-JUN-1993
  PRIOR APPLICATION DATA:
      APPLICATION NUMBER:  07/810782
      FILING DATE:  19-DEC-1991
  ATTORNEY/AGENT INFORMATION:
      NAME:  Love, Richard B.
      REGISTRATION NUMBER:  34,659
      REFERENCE/DOCKET NUMBER:  P0706P2P1D2
  TELECOMMUNICATION INFORMATION:
      TELEPHONE:  415/225-5530
      TELEFAX:  415/952-9881
      TELEX:  910/371-7168
INFORMATION FOR SEQ ID NO:  3:
  SEQUENCE CHARACTERISTICS:
      LENGTH:  1737 base pairs
      TYPE:  Nucleic Acid
      STRANDEDNESS:  Single
      TOPOLOGY:  Linear
US-08-802-627A-3
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Query Match       51.9%;    Score 974.4;  DB 2;  Length 1737;
Best Local Similarity  76.1%;    Pred. No. 1.2e-181;
Matches 1391;  Conservative   0;  Mismatches 301;  Indels 136;  Gaps  10;
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(Sequence alignment — Qy = Query, Db = Database — nucleotide sequence blocks with position numbers)

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Qy    50  GCAGGTAGCAGTGACCCTGAGGCGTTGGTGCTCCGGTAACCACCACGGCTGTAGAGC   109
Db    20  GCGCGGCGCAAAGTGACGCGCGAGGGCCTGAGTGCTGCCCAGTGCCACCGATCTGGAGAAC   79

Qy   110  GAGTGTTGCCATGGAACCGATCAGTCAGTGTGAGTATATACATTCTGATAACTACTCTGAAGA   169
Db    80  CAGCGGCGGTTACCATGGA------GGGGATCAGTATATACACTTCAGATAACTACACCGAGGA   134

Qy   170  AGTGGGGGTCTGGAGACTATGACTCAACAAGGAACCCTGCTTCCGGGATGAAAACGTCCA   229
Db   135  AATGGGGCTCAGGGGACTATGACTCCATGAAGGAACCCTGTTCCGTGGATGAAGAAATGTCTAA   194

Qy   230  TTTCAATAGGATCTTCCTGCCCACCACTCACTTCTTCATCATCTTCTTGACTGGCATAGTCGG   289
Db   195  TTTCAATAAAATCTTCCTGCCCACCACATCCTTCATCATCTTCTTAACTGGCATTGTGGG   254

Qy   290  CAATGGATTGGTGATCCTGGTCATGGTTACCAGAAGAGCTAAGGAGCATGACGACGACAA   349
Db   255  CAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAACTGAGAAGCATGACGACGACAA   314

Qy   350  GTACCGGCTGCACCTGTCAGTGGCTGACCTGGTACTTTGGGAAATTTTGTGTCATCACACTCCCCTTCTGGGC   409
Db   315  GTACAGGCTGCACCTGTCAGTGGCGACCTGGTACTTTTGTCATCACACGCGTTCCCTTCTGGGC   374

Qy   410  AGTTGATGCCATGGCCATGGTACTTGGGAAATTTGTGTAAGGCTGTCCATATCAT   469
Db   375  AGTTGATGCGTGCAAACTGGTACTTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCAT   434

Qy   470  CTACACTGTCAACCTCTACAGCAGCGTTCTCATCCTGGCCTTCATCAGCCTGGACCGGTA   529
Db   435  CTACACAGTCAACCTCTACACGCAGCAGTGTCCTCATCCTGGCCTTCATCAGTCCTGGCACCGCTA   494

Qy   530  CCTCGCCATTGTCACGCCACCACGCAACAGTCAAGGCCAAGGAAACTGCTGCTGAAAAGGC   589
Db   495  CCTCGCCATCGTCACGCCACCACGCAACAGTCAAGAGCCAAGGAAGCTGTTGGCTGAAAAGGT   554

Qy   590  AGTCTATGTGGGCGGCTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATTCTTTGC   649
Db   555  GGTCTATGTGGGCCGTCTGGATCCCTGCCCTCCTCCTGCTGACTATTCCCGACTATCATCTTTTGC   614

Qy   650  CGACGTCAGCAGCCAGGGGGGACATCAGTCAGGGGATGACAGGTACATCTGTGACCGGCCTTTA   709
Db   615  CAACG---------TCAGTGAGGCAGATGACAGATATCTGTGACCGGCCTTCTA   659

Qy   710  CCCGGATAGCCTGTGGATGGTGTGTTCAATTCCAGTTTCCAGTTGTTCCAGTTGTTCGTGTCATCCT   769
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Qy   830  GGGCCACCAGAAGGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTCATCCTTTCTTGC   889
Db   780  GGGCCACCAGAAGGCCAAGGCCCTCAAGACCCTCAAGACCATCCTCATCCTCGGCGGCTTTCTCGC   839

Qy   890  CTGCTGGCTGCCATTATGTGGGATCAGCAGCATCGACTCCTTCATCCTTTTGGGAGTCAT   949
Db   840  CTGTTGGCTGCCTTACTGAACCTTGGGATCAGCATCGACTCCTTCATCCTCTGGAAATCAT   899

Qy   950  CAAGCAAGGATGTGACTTCGAGACTGTGCACAAGTGGATCCTCATCACAGAGGCCCT   1009
Db   900  CAAGCAAGGGTGTGAGTTTGAGAACACTGTGCACAAGTGGCACAGTGCCAAATTCCATCACCGAGGCCCT   959

Qy  1010  CGCCTTCTTCCACTGTTGCCTGAACCCATCCTCTTCCTCGGGCGGCCAAGTTCAA   1069
Db   960  AGCTTTCTTCCACTGTTGCTGAACCCCATCCTCTATGCTTTCCTTGGGAGCCAAATTTAA   1019

Qy  1070  AAGCTCTGCCCAGCCATGCACTCAACTCCATGAGACGAGAGAGCTCCAGCCTCAAGATCCTTTC   1129
Db  1020  AACCTCTGCCCAGCCAGACGCACTCACCTCTGCGTCCGTCTCCAAGTCCAGCCTCAGAGATCCTCTC   1079

Qy  1130  CAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCGTGTTCATGTCTCAGACTCCAGTTTTCA   1189
Db  1080  CAAAGGAAAGCGAGGTGGAGCATTCATCGTTTTCATCGTCTTGTTCCACTGAGTCTCTTCAAGTTTTCA   1139

Qy  1190  CTCCAGCTAACCCTTATGCAAAGACTTATCAAAGACTTATATATTTTTTATATGATAACTAAAGAACTT   1249
Db  1140  CTCCAGCTAA-------CACAGTAAAAAGACTTTTTTTTATACGATAAAATAACTTT   1191

Qy  1250  TTTTATGTTACACATTTTCCAGATATAACGAACTGACAGTCTTGTACAGTTCTTTTTTTTTT   1309
Db  1192  TTTTAAGTTACACATTTTCAGATATAACGAACTGTACCAATATTGTACAGTTTTTTATTGC   1251

Qy  1310  TTTTTAATTGACTGTTGGGAGTTTATGTTCCTCAGTTTTGTGAGGTTTGACTTAATTT   1369
Db  1252  TTGTTGGATTTTGT------CTTGTGTTTCTTTAGTTTTTGTGAAGTTTAATTGACTTA   1305

Qy  1370  ATATAAATATTGTTTTTTTGTTGTTTCATGTGAATGAGCGTCTAGGCAGGACCTGTGGCC   1429
Db  1306  TTTATA---TAAATTTTTTTTTTTGTTTCATATTGCAATTGATGTGTGTCTAGGCAGGACCTGTGGCC   1361

Qy  1430  AAGTTCTTAGTAGCTGTGTTATCTGTGTAGGAGACTGTAGAGAGAAAACTGA   1489
Db  1362  AAGTTCTTAGTTGTCGTGTATGTCTCGTGGTAGGACTGTAGAA-------AAGGGAACTGA   1413

Qy  1490  ACATTCCAGAATGTCGTGTAAATTGAATAAGCTAAAGCTAGCCGTGATCCTGTTGCTGCA   1549
Db  1414  ACATTCCAGAGCGTGTAGTGAGTAGTCACGTAAAGCTAAAGCTAGCCAGCTGTTTATGCA   1473

Qy  1550  TAATCTCTTCATTCCGAGGAGCAGCACCCCCACCCCCACCCCCACCCCATTCTTAAAT   1609
Db  1474  TAGATAATCTCTCCA-----------------------------------   1488

Qy  1610  TGTTTGGTTATGCTGTGTGATGGTTGTTGGTTTTTTTTTGTTGTTGTTGTTTT   1669
Db  1489  -------------------TTCCCGTGGACGCGTTTTTCCTGTTCTTAAGACGTGAT   1525

Qy  1670  TTTTCTGTAAAAGATGGCACTTAAAAACCAAAGCCTGAAAATGGTGGTAGAAAATGTCGGGGT   1729
Db  1526  TTTGCTGTAGAAGATGGCACTTATAACCAAAGCCAAAGTGGT-ATAGAAATGCTGG---   1581

Qy  1730  TTTTTTTGTTTGTTTGTTGTTTTTCAGTTTTCAAGAGTAGATTGACTTCCTACAAAT   1789
Db  1582  -----------------TTTTTCAGTTTTCAGGAGTGGGTTGATTTCAGCACCTAC-AGT   1623

Qy  1790  GTACAGTCTTGTATTACAATTGTTAATAAAGTCAATGATAAACTTAAAAAAAAAAAA   1849
Db  1624  GTACAGTCTTGTATTAAGTTGTTAATAAAGTGTTAAACTTAAAAAAAAAAAAAA   1683

Qy  1850  AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA   1877
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Db        1684 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1711
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RESULT 7
US-08-801-238-3
; Sequence 3, Application US/08801238
; Patent No. 5919896
GENERAL INFORMATION:
  APPLICANT: Lee, James
  APPLICANT: Wood, William I.
  TITLE OF INVENTION: PF4A RECEPTOR
  NUMBER OF SEQUENCES: 6
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: 460 Point San Bruno Blvd
    CITY: South San Francisco
    STATE: California
    COUNTRY: USA
    ZIP: 94080
  COMPUTER READABLE FORM:
    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: WinPatin (Genentech)
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/801,238
    FILING DATE: 19-Feb-1997
    CLASSIFICATION: 530
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/284586
    FILING DATE: 10-AUG-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/076093
    FILING DATE: 11-JUN-1993
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 07/810782
    FILING DATE: 19-DEC-1991
  ATTORNEY/AGENT INFORMATION:
    NAME: Love, Richard B.
    REGISTRATION NUMBER: 34,659
    REFERENCE/DOCKET NUMBER: P0706P2P1D1
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 415/225-5530
    TELEFAX: 415/952-9881
    TELEX: 910/371-7168
  INFORMATION FOR SEQ ID NO: 3:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 1737 base pairs
      TYPE: Nucleic Acid
      STRANDEDNESS: Single
      TOPOLOGY: Linear
US-08-801-238-3

Query Match   51.9%;   Score 974.4; DB 2; Length 1737;
Best Local Similarity 76.1%;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps 10;

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Qy   50 GCAGGTAGCAGTGACCCTCTGAGGCGTTTGGTGCTCCGGTAACCACCAGGGCTGTAGAGC 109
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Db   20 GCGCGGCGCAAAGTGACGCGCGAGGGCCTGAGTGCTCCGAGTAGCCACCGCATCTGGAGAAC 79

Qy  110 GAGTGTTGCCATGGAACCGATCAGTGTGATATA----------CACTT 169
         ||||    |||  |   ||  | | | |  | |          |||||
Db   80 CACGGGGTTACCATGA-----GGGGATCAGTAGTATATACACTTCAGATT 134

Qy  170 AGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAACGTCCA 229
         | ||||| || || |||| ||||| |||||||||||||| ||||| |||||||| ||| |
Db  135 AATGGGCTCAGGGGACTATTGACTTCATGAGGAACCCTGTTTCCGTGAAGAAAATGCTAA 194

Qy  230 TTTCAATAGGATCTTCCTGCCCACCATTCCTGCCCACCACTCCTACTTCTTCATCATCTT 289
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Db  195 TTTCAATAAAATCTTCCTGCCCACCATCCATCCTCACTCACTCCATCATCTTCTTAACTGGCATTGTGGG 254
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Qy  290 CAATGATTGGTCATCCTGGTCATGGGTTACCAGAGAGAAGCTAAGGAGCATGACGACGACAA 349
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Db  255 CAATGATTGGTCATCCTGGTCATGGGTTACCAGAGAAGAAACTGAGAAGCATGACGACGACAA 314

Qy  350 GTACCGGCTGCACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGGGC 409
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Db  315 GTACAGGCTGCACCTGTCAGTGGCCGACCTCCTCTTTGTCATCACGGTCTTCCTTCTGGGC 374

Qy  410 AGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAGGCTGTCCATATCAT 469
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Db  375 AGTTGATGCCGGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCATGTCAT 434

Qy  470 CTACACTGTCAACCTTCTACAGCAGGTTCATCCTGGCCTTCATCAGCCTGGACCCGGTA 529
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Qy  530 CCTCGGCCATTGTCCACGCCACCACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGC 589
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Db  495 CCTGGCCATCGTCCACGCCACCACAGTCAAAGGCCAAGGAAGCTGTTGGCTGAAAAGGT 554

Qy  590 AGTCTATGTGGGCGTCTGGATGTCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTTGC 649
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Db  555 GGTCTATGTTGGCGTGTGGGTTGTGTTCAGCTTCCAGTTCCAGTTGGCCTTATCCTTATCCTTTGC 614

Qy  650 CGACGTCAGCCAGGCAGGGGGGACATCAGTCAGGGGGATGACAGGTACAGTCTGTGACCGCCTTTA 709
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Db  615 CAACG-------------TCAGTGAGGCAGATGACAGATATATCTGTGACCGCTCTA 659

Qy  710 CCCCGATAGCCTGTGATGGTGTGTTCAATTCCAGCATATAATGGTGGGTCTCATCCT 769
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Db  660 CCCCAATGACTTGTGGGTGGTTGTGTTCAGCTTCAGCACATCATGGTTGGCCTTATCCT 719

Qy  770 GCCCGGCATGCATCCTCCTGTTACTGACTGTCACACTCCAA 829
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Db  720 GCCTGTGTATTGTCATCCTGTCCGTGCATTGCATTATCATCTCCAAGTGTCACACTCCAA 779

Qy  830 GGGCCACCAGAAGCCAAGGCCCTCAAGACGACAGTCATCCTCATCCTAGCTTTCTTGC 889
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Db  840 CTGTTGGCTGCCTTACTACACATTGGGATCAGCGACTCGGACTCCTTCATCCTGGAAATCAT 899

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Db  960 AGTTTTCTTCCACTGTGTCTGAACCCCATCCTCATGCTTCATGCTTTCTGGGAGCCAAATTTAA 1019

Qy 1070 AAGCTCTGCCCAGCATGCACTCAACTCCATGAGCAGAGAGGCTCCAAGATCCTTTC 1129
         ||||||||||||| ||| ||||||| ||||||  |||||||| ||| |||||| ||
Db 1020 AACCTCTGCCCAGCACGCACTCACCTTCCGTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCC 1079

Qy 1130 CAAAGGAAAGCGGGGGTGGACACTCTTCCGCTCCCACCGGAGTCCAGAATCCTCCAGTTTCA 1189
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Db 1080 CAAAGAAAGGAAAGCGGAGGTGGACATTCATCATCGTTTCCACTGCTCTGAGTCTGAGTCTTCA 1139

Qy 1190 CTCCAGCTAACCCTTATGCAAAGACTTATACACTTCTGTAACTACTCTGAGA 1249
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Db 1140 CTCCAGCTAA-------CACAGTGTAAAGACTTTTTTTTATACGATAAATAACTTTT 1191

Qy 1250 TTTTATGTTACACATTTTCCAGATATAAGAGACTGACCAGTCTTGTACAGTTTTTTTTT 1309
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Db 1192 TTTTAAGTTACACATTTTTCAGATATAAAAAGACTGACCAATATTGTACAGTTTTTATTGC 1251

Qy 1310 TTTTTAATTGACTGTTGGGAGTTTATGTTCCTCAGTTTTGTGAGGGTTGACTTAATTT 1369
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Db 1252 TTGTTGGATTTTTGT-----CTTGTGTTTCTTTAGTTTTGTGAAGTTTAATTGACTTA 1305
```

NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D3
TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-5530
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
  LENGTH: 1737 base pairs
  TYPE: Nucleic Acid
  STRANDEDNESS: Single
  TOPOLOGY: Linear
US-08-801-228-3

Query Match   51.9%;   Score 974.4; DB 2;   Length 1737;
Best Local Similarity 76.1%;   Pred. No. 1.2e-181;
Matches 1391; Conservative 0; Mismatches 301; Indels 136; Gaps   10;

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Qy      50 GCAGTAGCAGTGACCCTCTGAGCCGTTGTGCTCCGGTAACCACCAGGCTGTAGAGC 109
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Qy     170 AGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGGAAAACGTCCA 229
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Db     135 AATGGGCTCAGGGGACTACTGACTCCATGAGGAGGAACCCCTGTTTCCGTGAAGAAAATGCTAA 194

Qy     230 TTTCAATAGGATCTTCCTGCCCACCATCTACTTCACTTCTTGACTGGCATAGTCGG 289
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Db     195 TTTCAATAAAATCTTCCTGCCCACCATCTACCTCCATCATCTTCTTAACTGGCATTGTGGG 254

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Db     255 CAATGGATTGGTCATCCTGGTCATGGGTACCAGAAGAAACTGAGAAGCATGACGGACAA 314

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Db     315 GTACAGGCTGCACCTGTCAGTGGCGTCTGGATCCCTCTTTGTCATCACACTCCCCTTCTGGGC 374

Qy     410 AGTTGATGCCATGGCATGGTACTTGGGAAATTTTGTGTAAGGCTGTCCATATCAT 469
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Db     375 AGTTGATGCCGTGGCAAACTGGTACTTTGGGAAACTTCCTATGCAAGGCAGTCCATGTCAT 434

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Db     495 CCTGGCCATCGTCCACGCCACCAACAGTCAGAGGCCAAGGAAGAAGTGTTGGCTGAAAAGGT 554

Qy     590 AGTCTATGTGGGCGTCTGACTACACCTGACTTCATCTTTGC 649
           || | |||| || |||||||||||||||||||||||||||| ||
Db     555 GGTCTATGTTGGGCGTCTGGATGGGTTGTTTCAGTTTCAGCACCATCATGGTTGGCCTTATCCTTTGC 614

Qy     650 CGACGTCAGCCAGGGGACATCAGTCAGGGGGATGACAGTACATCGTGACCGCCTTTA 709
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Qy     710 CCCCGATAGCCTGTGGATGGTGTTCAATTCCAGCATATAATGGTGGGTCTCATCCT 769
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Db     660 CCCCAATGACTTGTGGTGGTTGTTCAGTTTCAGCACCATCATGGTTGGCCTTATCCT 719

Qy     770 GCCCGGCATCGTCATCCTCTCGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAA 829
           |||| ||| |||||| |||||||||||||||||||||||||||||||||||||||
Db     720 GCCTGGTATTGTCATCCTGGTCATTGCATTATCATCTCCAAAGCTGTCACACTCCAA 779

Qy     830 GGGCCACCAGAAGGCCAAGGCCCTCAAGACGACAGCAGTCATCCTCATCCTAGTTCTTTGC 889
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Qy    1370 ATATAAATATTGTTTTTTGTTTGTTCATGTGAATGAGCGGTCTAGGCAGGACCTGTGGCC 1429
           |||| ||||   ||| | |||||||||||||||||||||||||||||| |||||||||||
Db    1306 TTTATA---TAAATTTTTTGTTTCATATTGATGTGTCTCTAGGCAGGACCTGTGGCC 1361

Qy    1430 AAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTAGAACTGTAGAGGGAGAAACTGA 1489
           ||||| |||||||||||| ||||||| |||||| ||||||      ||  ||||||||||
Db    1362 AAGTTCTTAGTTGCTGTATGTCTCGTGGTAGGACTGTAGAA-------AAGGGAACTGA 1413

Qy    1490 ACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTCCTCAGCTGTGTGCTGCA 1549
           |||||||||||  | | || ||| ||| || |||  || |||| || ||||||||||| |||
Db    1414 ACATTCCAGAGCGTGAGTAGTGAATCAACGTAAAGCTAGAAATGATCCCCAGCTGTGTTATGCA 1473

Qy    1550 TAATCTCTCATTCCGAGGAGCACCCCACCCCACCCCCACCCCCATTCTTAAAT 1609
           ||  ||||  ||||
Db    1474 TAGATAATCTCTCCA---------------------- 1488

Qy    1610 TGTTTGGTTATGCTGTGTGATGGTTTGGTTTTTGTTTTTTGTTGTTGTTGTTTTT 1669
           ||||||||| |||| |||||||||||||  ||||||||||||||||||||||||||||
Db    1489 --------------TTCCCGTGGGACGTTTTTTTCCTGTTCTTAAGACGTGAT 1525

Qy    1670 TTTTCGTAAAAGATGCACTTAAAACCAAAGCCTGAAATGGTGGTAGAAAATGCTGGGGT 1729
           ||| |||||||| |||||| | ||| | ||  ||||| || |||||||||||| ||||
Db    1526 TTTGCTGTAGAAGATGGCACTTATAACCAAAGCCCAAAGTGGT-ATAGAAATGCTGG--- 1581

Qy    1730 TTTTTTGTTTGTTTTTTCAGTTTTCAAGAGTAGATTGACTTCAGTCCCTACAAAT 1789
                      ||||||||||||| | |||| ||||| |||| ||||||||||||||
Db    1582 ----------TTTTTCAGTTTTTCAGGAGTTGGTTGATTTCAGCCACCTAC-AGT 1623

Qy    1790 GTACAGTCTTGTATTACATTGTTAATAAAGTCAATGATAAACTTAAAAAAAAAAAAAA 1849
           ||||||||| |||||||| |||||||||||| |||| | ||||||||||||||||||||||
Db    1624 GTACAGTCTTGTATTAAGTTGTTAATAAAGTACATGTTAAAACTTAAAAAAAAAAAAAAAAA 1683

Qy    1850 AAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
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Db    1684 AAAAAAAAAAAAAAAAAAAAAAAAAA 1711
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RESULT 8
US-08-801-228-3
; Sequence 3, Application US/08801228
; Patent No. 5922541
GENERAL INFORMATION:
 APPLICANT: Lee, James
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
 TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
  ADDRESSEE: Genentech, Inc.
  STREET: 460 Point San Bruno Blvd
  CITY: South San Francisco
  STATE: California
  COUNTRY: USA
  ZIP: 94080
 COMPUTER READABLE FORM:
  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/08/801,228
  FILING DATE: 19-Feb-1997
  CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/284586
  FILING DATE: 10-AUG-1994
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 08/076093
  FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 07/810782
  FILING DATE: 19-DEC-1991
 ATTORNEY/AGENT INFORMATION:

; Sequence 3, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
;   APPLICANT: Lee, James
;   APPLICANT: Wood, William I.
;   TITLE OF INVENTION: PF4A Receptors
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/104,296
;   FILING DATE: 24-June-1998
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/701265
;   FILING DATE: 22-AUG-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/664228
;   FILING DATE: 06-JUN-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/076093
;   FILING DATE: 11-JUN-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/810782
;   FILING DATE: 19-DEC-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Love, Richard B.
;   REGISTRATION NUMBER: 34,659
;   REFERENCE/DOCKET NUMBER: P0706P2C2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415/225-5530
;   TELEFAX: 415/952-9881
;   TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1737 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
US-09-104-296-3

Query Match   51.9%;   Score 974.4;   DB 3;   Length 1737;
Best Local Similarity   76.1%;   Pred. No. 1.2e-181;
Matches 1391; Conservative   0; Mismatches 301; Indels 136; Gaps 10;

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Qy    50 GCAGGTAGCAGTGACCCTCTGAGCCGTTGGTGCTCCGGTAACCACCACGGCTGTAGAGC 109
            |||| |||||||||||| |||  | ||| ||||||||| || |||| || || | ||||||
Db    20 GCGCGGCGCAAAGTGACGCCGAGGGCCTGAGTGCTCCAGTAGCCACCGGCCGCATCTGGAGAAC 79

Qy   110 GAGTGGTTGCCATGGAACCGATCAGTGAGTATATCACTTCTGATAACTACTCTGAAGA 169
            ||| | ||| ||||||     ||||||| | ||||||||| ||||||| ||| | |||
Db    80 CAGCGGTTACCATGGA-----GGGGATCAGTCATGTATATCACTTCAGATAACTACCACCGAGGA 134

Qy   170 AGTGGGGGTCTGGAGACTAGTGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAAGTCCA 229
            | |||| ||| ||||||||| |||||| |||| ||||| || |||| | |||||| ||||
Db   135 AATGGGCTCAGGGGACTATGACTCCATGAGGAGACCCTGTTTCCGTGAAGAAATGCTAA 194

Qy   230 TTTCAATAGGATCTTCCTGCCCACCATCACTTCTTCGACTGGCATGGCATAGTCGG 289
            ||||||||  |||||||||||||||||| || |||||   |||||| ||| || ||
Db   195 TTTCAATAAAATCTTCCTGCCCACCATCCATCATCTTCTTAACTGGCATTGGCATGACGGACAA 254

Qy   290 CAATGGATTGGTGATCCTGCGTTCATGGTTCACGGAGAAGCTAAGGAGAAGTCATGACGACGACACAA 349
            |||||||| |||||||||
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Db   780 GGGCCACCAGAAGCGCAAGGCCCTCAAGACCACCAGTCATCCTGCTTCTTCGC 839
Qy   890 CTGCTGGCTGCCATATTATGTGGGATCAGCATGCATCGACTCCTTTGGGAGTCAT 949
            |||| ||||||  | |  | || |||||||| ||| |||||||| |  |   |||
Db   840 CTGTTGGCTGCCTGCCTACTACATTGGGATCAGCATCGACTCCTCATCCTCCTGGAAATCAT 899
Qy   950 CAAGCAAGGATGTGACTTCGAGAGCACATTGTGCACAAGTGGATCTCCATCACAGAGGCCCT 1009
            |||||||| |||||| ||||| |   | ||||||||||||||| |||||||||| |||||||
Db   900 CAAGCAAGGTGTGAGTTTGAGACACTGTGCACAAGTGGATTTCCATCACCGAGGCCCT 959
Qy  1010 CGCCTTCTTCCACTGTTGCCTGACCCCATCCTTATGCCTTCCTCGGGGCCAAGTTCAA 1069
            | ||||||||||||| || |||||||||||| || |||| |||| | |||||||||||
Db   960 AGCTTTCTTCCACTGTGTCTGAACCCCTCATGCCTCTATGCTTGCTGGAGCCAAATTTAA 1019
Qy  1070 AAGGTCTGCCCAGCATGCACTCAACTCACTCCAGCTCAGCAGAGCGTCCAGCCTCAAGATCCTTTC 1129
            || ||||||||||| | || |||| | |  || ||| ||||| ||||||| ||| |||| |||| |
Db  1020 AACCTCGCCCCAGCAGCACGCACCTCACCTCTGTGAGCAGAGGTCCAGCCTCCAAGATCCTCTC 1079
Qy  1130 CAAAGGAAAGCGCGGGTGGACACTCTTCCGTCCTCCACGGAGTCAGAATCCTCCCAGTTTTCA 1189
            |||||||||| | | | |  ||| |  | ||| || ||||| | |||| | ||| |||| |||
Db  1080 CAAAGGAAAGCGAGGTGGCATTCATCTGTTTCCCACTGAGTCTGAGTCTCAAGTCTTCA 1139
Qy  1190 CTCCAGCTAACCCTTATGCAAAGACTTATATAATAATATATAATATATATGATAAAGAACTT 1249
            ||||||||||    |            |||||| |   | |  |  |  | ||||||| ||||
Db  1140 CTCCAGCTAA-------CACAGATGTAAAAGACTTTTTTTATACGATAAAATAACTTTT 1191
Qy  1250 TTTATGTTACACATTTTCAGATATAAGAGACTGACCAGTCTTGTACAGTTTTTTTTTTTT 1309
            ||| | ||||||| |||||| |||||||| | ||||| ||||||| |||||| | | |||
Db  1192 TTTAAGTTACACATTTTTCAGATATAAAAGACTGACCAATATGTACAGTTTTTTATTGC 1251
Qy  1310 TTTTTAATTGACTGTTGGGAGTTTATGTCCTCAGTTTTGTGAGGTTTGACTTAATTT 1369
            || || ||||||  |  | | ||| |||||||| ||| |||||||| ||  | |||
Db  1252 TTGTTGGATTTTTGT------CTTGTGTTTTGTTTTGTGAAGTTTAATTGACTTA 1305
Qy  1370 ATATAAAATATTGTTTTTGTTCATGTGAATGAGCCTCAGGCAGCAGGACCTGTGGCC 1429
            | | |||| | |||||||| ||| |||| |||||| |||||||||||| || || ||
Db  1306 TTTATA----TAAATTTTTTGTTCATATTGATGTGTCTCAGGCAGGACCTGTGGCC 1361
Qy  1430 AAGTTCTTAGTAGCTGTGTTATCTGTGTAGGACTGTAGAAACTGATCAAGGGAACTGA 1489
            |||| |||| | |||| || ||| || ||||    |  |||  ||||||||||||||
Db  1362 AAGTTCTTAGTGCTGTATGCTCGTGGTAGGACTGTAGAA-------AAGGGAACTGA 1413
Qy  1490 ACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTTGCTGCA 1549
            |||||||||||| ||||  | || ||| |||||  || ||| |||||||||| || |||
Db  1414 ACATTCCAGAGCGTGTAGTGAATCACGTAAAGCTAAAGATCACCCAGCTGTTTTATGCA 1473
Qy  1550 TAATCTCTTCATTCCGAGAGGAGCACCCCACCCCCCCACCCCCAATTCCTTAAAT 1609
            |||| ||  |  ||| | |||| |||||||||||
Db  1474 TAGATAATCTCTCCA---------------------------------- 1488
Qy  1610 TGTTTGGTTATGCTGTGTGATGGTGTTTTTTTTTGTTTGTTGTTGTTGTTTTTT 1669
               |  |    ||||  ||| | | ||| | ||| ||||  |||| ||| | |||
Db  1489 -----------------------------TTCCCGTGGAACGTTTTCCTGTTCTTAAGACGTGAT 1525
Qy  1670 TTTCTGTAAAAGATGGCACTTAAAACCAAAGCCTGAAATGGTGTGTAGAAATGCTGGGGT 1729
            ||| || ||| ||||||||| ||||||  |||| ||||| ||||| || ||| |||| |
Db  1526 TTTGCTGTAGAAGATGGCACTTATACCAAGAGCCCAAGTGGGT-ATAGAAATGCTGG--- 1581
Qy  1730 TTTTTTGTTTGTTTGTTTGTTCAGTTTGTTTCAAGAGTAGATTGACTTCAGTCCCTACAAAT 1789
            ||||||
Db  1582 -------------TTTTCAGTTTTTCAGGAGGTGGGTTGATTTCAGCACCTAC-AGT 1623
Qy  1790 GTACAGTCTTGTATATACATTGTTAATAAAAGTCAATGATAAAGTTAAAAAGAAAAAAAAAAA 1849
            | ||||| | |||  |    | ||| |||||  |  |||||| |||||| |||||||||||||
Db  1624 GTACAGTCTTGTATTAAGTTGTTTAATAAAAGTACATGTTTAAACTTAAAAAAAAAAAAAAAA 1683
Qy  1850 AAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
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Db  1684 AAAAAAAAAAAAAAAAAAAAA 1711
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RESULT 9
US-09-104-296-3

Db 255 CAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAACTGAGAAGCATGACGGACAA 314
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Qy 350 GTACCGGCTGCACCTGTCAGTGGCTGACCTGCTGTCATCACACTCCCCTCTCGGGC 409
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 315 GTACAGGCTGCACCTGTCAGTGGCTGACCTGCTGTCATCACGCTTCCCTCTCTCGGGC 374

Qy 410 AGTTGATGCCATGCCATGGTACTTTGTGGAAATTTTGTTGTAAGGCTGTCCATATCAT 469
         ||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db 375 AGTTGATGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCAT 434

Qy 470 CTACACTGTCAACCTCTACAGCAGCGGTTCTCATCCTGGCCTTCATCAGCCTGACCGGTA 529
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Db 435 CTACACAGTCAACCTCTACAGCAGCGTCCTCATCCTGGCCTTCATCAGTCTGACCGGCTA 494

Qy 530 CCTCGGCCATTGTCCACGCCACCAACAGTGCAAGGCCAAGGAAACTGCTGGCTGAAAAGGC 589
         |||||||||||||||||||||||||||||||||||||||||||||
Db 495 CCTGGGCCATCGTCCACGCCACCAACAGTGCAGAGGCCAAGGAAGCTGGCTGAAAAGGT 554

Qy 590 AGTCTATGTGGGGGTCTCGATCCCCAGCCCTCCTGACTATACCTGACTTCATCTTTGC 649
         |||||||||||||||||| ||||||||||||| |||||||||||||||||
Db 555 GGTCTATGTGGGGCTTGACTTCCTGATCCTGTGACTTCCTGACTTCATCTTTGC 614

Qy 650 CGACGTCAGCCAGCGGGGACATCAGTCAGGGGATGACAGGTACATCTGTGACCGCCTTTA 709
         |||||||
Db 615 CAACG   TCAGTGAGCGAGATGACAGATAGTCTGTGACCGCCTTCTA 659

Qy 710 CCCCGATAGCCTGTGGGATGTGGTGTTTCAATTCCAGCTATATAATGTGGGTCTCATCCT 769
         |||||||||||||||||||||||||||||||||||||||||||
Db 660 CCCCAATGACTTGTGGGGTGGTGTTGTGTTCCAGTTTCAGCATCATCATCTCTAAGCTGT 719

Qy 770 GCCCGGCATCGTCATCCTCCTCCTGTACTGCATCATCATCTCTAAGCTGTCACACTCCAA 829
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 720 GCTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCAA 779

Qy 830 GGGCCACCAGAGACGCAAGGCGCTCAAGACGCAGACCTTCATCCTCCTAGCTTTCTTTGC 889
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Db 780 GGGCCACCAGAGCAGGCCAAGGCGCCCCTCAAGACAGTCCTCATCCTCGGCTTCTTTCGC 839

Qy 890 CTGCTGGCTGCCATATTATGTGGGATCAGCATCGACTCCTTCATCCTTTTGGGAGTCAT 949
         ||||||||||||| |||||| ||||||||||||||||||| |||||
Db 840 CTGTTGGCTGCCTTACTACACATTGGGATCAGCATCAGCAATCATCCTCCTCTGGAAATCAT 899

Qy 950 CAAGGCAAGGATGTGACTTCGAGAGCATTGTGCACAAGGCCCT 1009
         ||||||||||||||||||||||||||||||||||||||||||
Db 900 CAAGGCGGTGTGAGTTTGAGAGCACTTGTGCACAAGTGGACTTCCATCACCGAGGGCCCT 959

Qy 1010 CGCCTTCTTCCACTGTTGCCTGAACCCCATCCTCTATGCCTTCCTGGGGCCCAAGTTCAA 1069
          |||||||||||||||||||||||||||||||||||||| |||||
Db 960 AGTCTTCTTCCACTGTTGTCTGAACCCCATCTGTTTCCTTGGAGCCCAAATTTAA 1019

Qy 1070 AAGCTCTGCCCAGCCATGCAGCACTCAACTCCATGAGCGAGAGCCTCAAGATCCTTTC 1129
          ||||||||||||||| ||||||||||||||||||||||| ||||||||||
Db 1020 AACCTCTGCCCAGCCACGCACTCACCCTGTGAGCAGAGGGTCCAGCGCCTCAAGATCCCTCTC 1079

Qy 1130 CAAAGGAAAGCGCGGGGTGGACACTCTTCCGGTCTCCACGGAGTCAGAATCCTCCAGTTTTCA 1189
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1080 CAAAGGAAAGCGAGGGTGGACATTCATCATCCACTGAGTCTGAGTCTTCAAGTTTTCA 1139

Qy 1190 CTCCAGCTAACCCTATGCAAAGACTTATATAATATATATATATATATATATGATAAAGAACTT 1249
          ||||||||||||||||||
Db 1140 CTCCAGCTAA   CACAGATGTAAAAGACTTTTTTTATACGATAAATAACTTTT 1191

Qy 1250 TTTATGTTACACATTTTCCAGATATAGAGAGACTGACCAGTCTTGTACAGTTTTTTTTT 1309
          |||||||||||||||||||||||||||||||||||||||||||
Db 1192 TTTTAAGTTACACATTTTTCAGATATAAAAAGACTGACCAATATTGTACAGTTTTTATTGC 1251

Qy 1310 TTTTTAATTGACTGTTGGGAGTTTATGTTCCTCAGTTTTTGTGAGGTTTGACTTAATTT 1369
          |||| ||| ||||||||||||||||||||||||||
Db 1252 TTGTTGGATTTTTGT   CTTGTGTTTCTTTAGTTTTTGTGAAGTTTAATTGACTTA 1305

Qy 1370 ATATAAATATTGTTTTTGTTTCATGTGAATGAGCGTCTAGGCAGGACCTGTGCC 1429
          |||| |
Db 1306 TTTATA   TAAATTTTTTTGTTTTGTTTCATATTGATGTGTGTCTAGGCAGGACCCTGTGCC 1361

Qy 1430 AAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTAGAACTGTGAGAGAGAAGAAACTGA 1489
          |||||||||||||||||||||||||||||||||||||||||
Db 1362 AAGTTCTTAGTTGCTGTATGTCTCCGTGGTAGGACTGTAGAA   AAGGGAACTGA 1413

Qy 1490 ACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTGTGCTCGCA 1549
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Db 1414 ACATTCCAGAGCGTGTAGTGAATCACGTAAAGCTAGAAATGATCCCCAGCTGTTTATGCA 1473

Qy 1550 TAATCTTCTTCATTCCGAGGAGGAGCACCCCACCCCCACCCCCATTCTTAAAT 1609
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Db 1474 TAGATAATCTCTCA   1488

Qy 1610 TGTTTGGTTATGCTGTGTGATGGTTGTTTGGTTTTTTTTGTTTGTGTTGTTTTTT 1669
          |||||||
Db 1489   TTCCCGTGGAACGTTTTCCTGTTCTTAAGACGTGAT 1525

Qy 1670 TTTTCTGTAAAAGATGGCACTTAAAACCAAAGCCTGAAATGGTGGTAGAAAATGCTGGGGT 1729
          ||||||||||||||| |||||||||||||||||||
Db 1526 TTGCGTGTAGAAGATGGCACTTATAAACCAAAGCCCAAAGTGGT ATAGAAAATGCTGG   1581

Qy 1730 TTTTTTGTTGTTTGTTGTTTTGTTTTTCAGTTTTCAAGAGTAGATTGACTTCAGTCCCTACAAAT 1789
          |||||||||||||
Db 1582   TTTTTCAGTTTTTCAGGAGTGGGTTGATTTCAGCACCTAC-AGT 1623

Qy 1790 GTACAGTCTTGTATTACATTGTTAATAAGTCAATGATAAAACTTAAAAAAAAAAAAAA 1849
          |||||||||||||||||||||||||||||||||||||||
Db 1624 GTACAGTCTTGTGTTATTAAGTTGTTAATAAAGTACATGTTAAACTTAAAAAAAAAAAAAAAA 1683

Qy 1850 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
          |||||||||||||||||||||||||||||||||||
Db 1684 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1711

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; SEQUENCE CHARACTERISTICS:
;   LENGTH:   1737 bases
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
PCT-US94-06380-2

Query Match     51.9%;   Score 974.4;  DB 6;   Length 1737;
Best Local Similarity   76.1%;   Pred. No. 1.2e-181;
Matches 1391;  Conservative   0;  Mismatches 301;  Indels 136;   Gaps  10;

Qy     50  GCAGGTAGCAGTGACCCTGAGGCGTTGGTGCTCCGGTAACCACCACGGCTGTAGAGC   109
           |||  ||||  || ||  |||| ||  ||||||||||| ||| ||  |||| ||
Db     20  GCGCGGCCGCAAAGTGACGCGCCGAGGGCCTGAGTGCTCCACCGCATCTGGAGAAAC    79

Qy    110  GAGTGTTGCCATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTTCTGAAGA   169
           || ||||||||||||||||  |||||||||||||||| |||||| ||||||||||
Db     80  CAGCCGGTTACCATGGA------GGGGATCAGTATATACACTTCAGATAACTACACCGAGGA   134

Qy    170  AGTGGGGTCTGGAGACTATGACTCCAACAAGGAGAACCCTGCTTCCGGGATGAAAAACGTCCA   229
           |||||||||||||||||| || ||||||||||||||| ||||| |||||||| ||||||||||
Db    135  AATGGGCTCAGGGGACTATGACTCCATGAAGGAAGCCCTGTTTCCGTGAAGAAAATGCTAA   194

Qy    230  TTTCAATAGGATCTTCCTGCCACCATCTACTTCTGATCATCTTCTTGACTGGCATAGTCGG   289
           |||||||  ||| ||||||||||||||||| ||||||||||||| |||||||||||||||||
Db    195  TTTCAATAAAATCTTCCTGCCACCATCTACTTCTCATCTTCTTAACTGGCATTGTGGG   254

Qy    290  CAATGGATTGGTGATCCTGGTCATGGTACCAGGAGAGCTAAGGAGCATGACGGACAA   349
           |||||||||||||||| |||||||||||||||||| ||||||||||||||||||||||
Db    255  CAATGGATTGGTCATCCTGGTCATGGGTTACCAGAGAAACTGAGAGCATGACGGACAA   314

Qy    350  GTACCGGCTGCACCTGTCAGTGGCTGACTGTGTACTTTGGGAAATTTTGTGTAAGGCTGTCCATATCAT   409
           ||||| |||||||| ||||| |||||||||  ||| |||||||  |||| | |||||||||||||||||
Db    315  GTACAGGCTGCACCTGTCAGTGGCCGACCTTGTCATCACTCCCCTTCCCTTCTGGGC   374

Qy    410  AGTTGATGCCATGGCGTCGGAATGGCAAACTGGTACTTTGGGAAATTTTGTGTAAGGCTGTCATATCAT   469
           |||||||||||| |||||||| |||| ||  ||||||| | |||| |||| ||||||||||||| |||||
Db    375  AGTTGATGTGGCCGTCAAACTGGTACTTTGGGCAAACTGGTACTTTGGCTGTCAAGGCAGTCAGTCAT   434

Qy    470  CTACACTGTCAACCTCTACAGCAGGCGTTCTCATCCTGGCCTTCATCAGCCTGGACCGGTA   529
           |||||| ||||||| |||||||||||| ||||||| |||||| |||||||||||||||
Db    435  CTACACAGTCAACCTCTACAGCAGTGTCCTCTCATCCTGGCCTTCATCAGCCTGGACCGCTA   494

Qy    530  CCTCGCCATTGTCCACGCCACCACCAACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGC   589
           |||||||||| || |||||||||||||||||| || |||||||||| |||| |||||||||||
Db    495  CCTGGCCATCGTCCACGCCACCACCAGTCAGAGGCCAAGGAAGGCTGTTGGCTGAAAAGGT   554

Qy    590  AGTCTATGTGGGCGTCTGGATCCCAGCCCTTCTCCTGCCCTTCTCGACTTCATCTTTGC   649
           |||||||||||| || |||||||||| |||||| ||| || ||||| ||||||||||
Db    555  GGTCTATGTGGGCGTCTGGATCCCGTCCCCCTGCTATTCCCGACTTCATCTTTGC   614

Qy    650  CGACGTCAGCCAGGGGACATCAGTGACAGTGCAGTCTCTTCAGCGGCGCTTTA   709
           ||||||||||| |||||||| |||||||||| || ||||| ||||||||| ||
Db    615  CAACG--------TCAGTGAGGCAGCAGATGACAGATATCGTGACCGCTTCTA   659

Qy    710  CCCCGGATAGCCGTGTGGATGGTGGTGCGTCCAGTTTCAATTGCACCATCATCTGTCATCCT   769
           |||||| || ||||||| || |||||||||||||||| || ||| ||||||||| |||||
Db    660  CCCCAATGACTGTGGTGGTGTTTGTTCCCAGTTTCAGTTTCAATTGCATTATCATCTCCAAG   719

Qy    770  GGGCCACCAGAAGCCCAAGGCCCTCCAAGACGACAGTCATCCTCCAGCTGTCTTCTTTGC   829
           |||| ||||||||  ||| |||||||| |||||||||| |||||| ||||| ||||| ||
Db    720  GCCTATGTGTCATCCTGTATTCCTGCTATTGCATTATCATCCAGCGTCACACTCCAA   779

Qy    830  GGGCCACCAGAAGCCCAAGGCCCTCCAAGACGACAGTCATCCTCCAGCTGTCTTCTTTGC   889
           |||||||||||||||||||||||||| ||| |||||||||| |||| |||| |||||| |
Db    780  GGGCCACCAGAAGCCGCAAGGCCCTCCAAGACCGACATCCTCCATCTCCTGGCTTTCTTCGC   839

Qy    890  CTGCTGGCTGCCATTATGTGGGAGTCATTTTGGGAGTCAT   949
           ||||| |||| |||| | || ||||| || ||||||||||
Db    840  CTGTTGGCTGCCCTTACTACATTGGGATCTCCTCCTGGAAATCAT   899

Qy    950  CAAGCAAGGATGTGACTTCGAGAGACATTGTGCACAAGTGGATCTTCATCACCAGAGGCCCT   1009
           |||||||| ||||| |||||||||||| ||
Db
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Db    900  CAAGCAAGGGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCCATCACCGAGGGCCCT    959

Qy   1010  CGCCTTCTTCCACTGTGCCTGAGTGCTCCATCCCATCCTATGCCTTCCTCGGGGCCAAGTTCAA   1069
           ||||| |||||||| || ||||| |||||| |||||||| |||  ||||||||||||||||||
Db    960  AGCTTTCTTCCACTGTGTCTGAACCCCATCCCATCTTCCTATGCTTTCCTTGGAGCCAAATTTAA   1019

Qy   1070  AAGCTCTGCCCAGCATGCACTCAACTCCATGCATGAGCAGAGCTCCAAGATCCTTTC   1129
           |||||||| ||||| ||||| | ||| || ||||||| |||||| |||| || |||
Db   1020  AACCTGTCCCCAGCACCACCTCGTGAGCGAGCAGAGGGTCCAGCCTCAAGATCCTCTC   1079

Qy   1130  CAAAGGAAAGCGGGGGTGGACACTCTTCCGTCTCCACGAGTCAGAATCCTCCAGTTTCA   1189
           ||||| |||||| ||| ||||| || |||||||||  | |||  |||| |||||||||
Db   1080  CAAAGGAAAGCGAGGTGGACATTCATCTGTTCCACTGAGTCTGAGTCTTCAAGTTTTCA   1139

Qy   1190  CTCCAGTAACCCTTATGCAAAGACTTATATATAATATATATATGATAAAGAACTT   1249
           ||  ||| ||  || |||||| | ||||||| |  ||| || || ||||||  ||
Db   1140  CTCCAGCTAA-------CACAGATGTAAAAGACTTTTTTTTTATACGATAAATAAACTTTT   1191

Qy   1250  TTTTATGTTACACATTTTCCAGATATAAGACTGACCAGTCTTGTACAGTTTTATTGC   1309
           |||||| || |||| | |||| ||  || ||||| |||||| ||  |||| ||||||
Db   1192  TTTAAGTTACACATTTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTTTATTGC   1251

Qy   1310  TTTTTAATTGACTGTTGGGAGTTTATGTTCCTCTAGTTTTGTGAGGTTTGACTTAATTT   1369
           | |||||| || || | | ||| ||||||| || |||||||| ||||| || ||||
Db   1252  TTGTTGGATTTTGT------CTTGTGTTTCTTTAGTTTGTGGAAGTTTAATTGACTTA   1305

Qy   1370  ATATAAAATATTGTTTTTGTTTTGTTTCATGTGAATGAGCGTCTAGGCAGGAGGAAGAAACTGA   1429
           ||||  ||||||||||||||||||||  |||||  |  ||||| |||||||||
Db   1306  TTTATA----TAAATTTTTTTTGTTTCATATTGATGTCGTGGTAGGACTGTAGA--------AAGGGAACTGA   1361

Qy   1430  AAGTTCTTAGTAGCTGTGTTTATCGTGTGTAGGACTGTAGAACTGTAGCCGTGATCCTCAGTCGTTGTGCTGCA   1489
           |||||||  | ||| |||||||  |  | || ||| || |||||| ||||  |||||||||||||| |||| ||
Db   1362  AAGTTCTTAGTTGCTGTATGTCGTGTGGTAGGACTGTAGA-------AGGGAACTGA   1413

Qy   1490  ACATTCCAGAATGTGTGTAAATTGAATAAAGCTAGCCGTGATCTCCAGTCGTTGTGCTGCA   1549
           ||||||||||||||||| ||||||||||||||||||  | ||||||| |||| ||||| ||
Db   1414  ACATTCCAGAGCGTGTAGTGAATCACGTAAAGCTAAAGTCAGTCTAGAAAGCTAGAAAATGATCCCCAGCTGTTTATGCA   1473

Qy   1550  TAATCTCTTCATTCCGAGGAGGAGCACCCCACCACCCCCATTCTTAAAT   1609
           ||  ||| | ||| ||
Db   1474  TAGATAATCTCTTCCA--------------------   1488

Qy   1610  TGTTTGGTTATGCTGTGTGATGGTTGTTTTGGTTTTTGTTGTTGTTGTTTTTT   1669
           ||||  || ||  |||||| ||||||| ||| || ||| || |||||||||||
Db   1489  --------------TTCCCGTGGAACGTTTTTCCTGTTCTTAAGACGTGAT   1525

Qy   1670  TTTTCTGTAAAGATGCGCACTTAAAACCAAGCCTGAAATGTGTGGTAGAAATGCTGGGGT   1729
           ||||| ||| | | | |||||| |||||||| ||  ||||||| || ||  ||||||
Db   1526  TTTGCTGTAGAAGATGGCACTTATAACCAAAGCCCAAAGTGGT-ATAGAAATGCTGG---   1581

Qy   1730  TTTTTTTGTTTTGTTGTTTTTTCAGTTTTCAAGAGTTGACTTCAGTCCTACAAAT   1789
           ||||||| |||||  |||||   ||||| || |||| ||| |||| || |||
Db   1582  --------------TTTTTCAGTTTTTCAGGAGTGGTGTGATTTCAGCACTTAC-AGT   1623

Qy   1790  GTACAGTCTTGTATTACATTGTTAATAAAGTCAATGATAAACTTAAAAAAAAAAA   1849
           ||||||||||| || |||| | ||||| |||||  | ||| || |||||||||||
Db   1624  GTACAGTCTTGTTATTAAGTTGTTAATAAAGTTGTTAATAAACTTAAAAAAAAAAAA   1683

Qy   1850  AAAAAAAAAAAAAAAAAAAAAAAAA   1877
           |||||||||||||||||||||
Db   1684  AAAAAAAAAAAAAAAAAAAAAAA   1711
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RESULT 11
US-09-517-605-14
; Sequence 14, Application US/09517605
; Patent No. 6391567
; GENERAL INFORMATION:
;   APPLICANT: Littman, Dan R.
;   APPLICANT: Kwon, Douglas S.
;   APPLICANT: van Kooyk, Yvette
;   APPLICANT: Geijtenbeck, Theo
;   TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO

```
;   TITLE OF INVENTION: CELLS
;   FILE REFERENCE: 1049-1-017
;   CURRENT APPLICATION NUMBER: US/09/517,605
;   CURRENT FILING DATE: 2000-03-02
;   NUMBER OF SEQ ID NOS: 17
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 1679
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-517-605-14

Query Match       50.8%;  Score 952.8; DB 3;  Length 1679;
Best Local Similarity  80.2%;  Pred. No. 2.1e-177;
Matches 1210;  Conservative  0;  Mismatches 252;  Indels  46;  Gaps  6;

Qy       44  GCAGGTCAGGTAGCAGTGACCCTGAGCGGTGTTGGTGCTCCGGTAACCACCACGGGCTG  103
                |||||||||||||| ||||  |||||||||  || ||||| |||||| |||
Db       12  GCGCGCAGCAGGTAGCAAAGTGACAGCCGAGGGCCTGAGTCTGCCAGTAGCGCCATCTG   71

Qy      104  TAGAGCGAGTGCGTGTGCCATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTC  163
                |||||||  |  |  |  ||||| | | ||||||||||||
Db       72  GAGAACCAGCGCGGTTACCATGGA-----GGGGATCAGTATATACACTTCAGATAACTACAC  126

Qy      164  TGAAGAAGTGGGGCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAA  223
                ||||||  || |||||||  ||| |||| ||| || ||  ||| ||||||||||||
Db      127  CGAGGAAATGGGCTCAGGGACTATGACTCCATGGAAGGGACCCTGTTCCGTGAAGAAAA  186

Qy      224  CGTCCATTTCAATAGGATCTTCCTGCCCACCATCTACTTCATCATCTTCTTGACTGGCAT  283
                ||||| |||||| | ||| ||||||||||||||||| ||||||| |||| || |||||||
Db      187  TGCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTTCATCATCTTCTTAACTGGCAT  246

Qy      284  AGTGTCGGCAATGGATTGGTGATCCTGGTCATGGGTTACCAGAGAAGCTAAGGAGCATGAC  343
                ||||  ||||||||||||||| ||||| |||||||||||| |||||| |||| ||||||
Db      247  TGTGTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGGAAACTGAGAAGCATGAC  306

Qy      344  GGACAAGTACCGGCTGCACCTGTCAGTGGCTGACCTCTTTGTCATCACACTCCCCTT  403
                ||||||||||||||| |||||||||||||||| |||||||||||||||||| ||||||
Db      307  GGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCTTTGTCATCACACTCCCTT  366

Qy      404  CTGGGCAGTTGATGCCGGTGCAAACTGGTACTTTGGGAAATTTTGTGTGAAGGCTGTCCA  463
                ||||||||||| ||| |||||||||||||| ||||||||  ||||| ||||||||||||
Db      367  CTGGGCAGTTGATGCCGGTGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCA  426

Qy      464  TATCATCTACACTGTCAACCTGTACAGCAGCGTTCTCATCCTGGCCTTCATCAGCCTGGA  523
                ||||| ||||||||| |||||||| |||||||| ||||||||||||||||||| |||||
Db      427  TGTCATCTACACACAGTCAACCTCTACAGCAGCGTGTCCTATCCTGGCCTTCATCAGTCTGGA  486

Qy      524  CCGGTACCTGGCCATTGTCCACGCCACCAACAGTCAAAGCCAAGGAAACTGCTGGCTGA  583
                ||||||||||| |||||||||||||||||||||||||||||| ||||||||| |||||
Db      487  CCGCTACCTGGCCATCGTCCACGCCACCAACAGTCAGAGGCCAAGGAAGAGCTGTTGGCTGA  546

Qy      584  AAAGGCAGTCTATGTGGGCGATCGTCATCCTCTCCGTTACTGACTATACCTGACTTCAT  643
                |||||  ||||||| ||||| ||| |||||||||||||||||| || ||||||||||||
Db      547  AAAGGTGGTCTATGTTGGGCGTCTGATCCCTGCCCTCCTGCTGCTATTCCCGACTTCAT  606

Qy      644  CTTTGCCGACGTCAGCCAGCCCAGGGGACATCAGTCAGGGGATGACAGGTACATCTGACCG  703
                ||||||||| |       ||| ||||||||||||||||| || |||||||||||||||
Db      607  CTTTGCCAACG----------TCAGTGAGGCGACGATGACAGATATATCTGTGACCG  651

Qy      704  CCTTACCCCGATAGCCTGTGGATGGTGGTGTTTCAATTCCAGCATATAATGGTGGGTCT  763
                | |||||||||| |||||| ||||||||||||  |||||||  |||||| ||| |||||
Db      652  CTTCTACCCCAATGACTTGTGGGTGGTTGGTGTGTTCCAGTTTCAGCACATCATGGTTGGCCT  711

Qy      764  CATCCTGCCCGGCATCGTCATCCTCTCCGTTACTGCATCATCATCTCTAAGCTGTCACA  823
                |||||||||||| ||||||||||||||||||| | | |||||| ||||||| |||||||
Db      712  TATCCTGCTGGTATTGTCCTCCGTATTGCATTATCATCTCCAAGCTGTCACA  771

Qy      824  CTCAAGGGCCACCAGAAGCGCCAGAGCGCCAAGGCCCTCAAGACGCAGTCATCATCCTAGCTTT  883
                || ||||||||||||||| |||||||| |||||||||||||||||||||||||||||| |||||
Db      772  CTCCAAGGGCCACCAGAAGCGCAAGGCGCCCAAGAGCACCAGTCATCATCCTCATCCTGGCTTT  831

Qy      884  CTTTGCCTGCTGGCTGCCATATTATGTGGGGATCAGCATCGACTCCTTCATCCTTTTGGG  943
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Qy      944  AGTCATCAAGCAACGAGATGACTTCGAGAGCAGCATTGCACAAGTGGATCTCCATCACAGA  1003
Db      892  AATCATCAAGCAAGGGGTGTGAGTTTGAGATTTGAGACACTGCACAAGTGGATTTCCATCACCGA  951

Qy     1004  GGCCCTGCCTTCTTCCACTGTTGCCTGAGCACCCATCCTCTATGCCTTCCTCGGGGCCAA  1063
Db      952  GGCCCTAGCTTCTTCCACTGTTCTGAGCACCCATCCTCTATGTCTTCCTTGGAGCCAA  1011

Qy     1064  GTTCAAAAGCTCTGCCCAGCATGCATGCAGCACTCAACTCCATGAGCAGAGGCTCAGCCTCAAGAT  1123
Db     1012  ATTTAAAAACCTCTGCCCAGCACCACTCACCTCTGTGAGCAGAGGGGTCCAGCCCTCAAGAT  1071

Qy     1124  CCTTTCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCCACGGAGTCAGAATCCTCCAG  1183
Db     1072  CCCTTCCAAAGGAAAGCGAGGGTGGACAATTCACCTTCATCTGTCTGTTCCACTGAGTCTTCAAG  1131

Qy     1184  TTTTCACTCCAGCTAACCTTATGCAAAGACTTATATATATATATATGATAAA  1243
Db     1132  TTTTCACTCCAGCTAACACAGTGTAAAAGACTTTT-------TTTATACGATAAATA  1183

Qy     1244  GAACTTTTTATGTTACACATTTTCCAGATATGAAGAGACTGACCAGTCTGACAGTCTGTACAAGTTTT  1303
Db     1184  ACTTTTTTTAAGTTACACATTTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTT  1243

Qy     1304  TTTTTTTTTTTTTAATTGACTGTTGGGAGTTTATGTTCCTCTAGTTTTTTGTGAGGTTTGACT  1363
Db     1244  TATTGCTTGTTGGATTTTTTGT-----CTTGTGTTTCTTTAGTTTTTTGTTGAAGTTTAATT  1297

Qy     1364  TAATTTATATAAATATTGTTTTTTGTTTCATGTGAATGACGGCGTCTAGGCAGGACCT  1423
Db     1298  GACTTATTTATA---TAAATTTTTTTTGTTTCATATTGATGTGTGTCTAGGCAGGACCT  1353

Qy     1424  GTGGCCAAGTTCTTAGTAGCTGTTTATCTGTCGTAGGACTGTAGGAACTGTAGGAGGAAGA  1483
Db     1354  GTGGCCAAGTTCTTAGTTGCTGTATGTCTCGTGATGTGTAGGACTGTAGAA-------AGGGG  1405

Qy     1484  AACTGAACATTCCAGAAATGTGTGGTAAATTGAATGAAGAGCCGTGATCCTCAGCTGTT  1543
Db     1406  AACTGAACATTCCAGAGCGTGAGTGAGTAGTAGAAATGATCCCCAGCTGTT  1465

Qy     1544  GCTGCATA  1551
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Db     1466  TATGCATA  1473
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RESULT 12
US-09-582-224A-5
; Sequence 5, Application US/09582224A
; Patent No. 6429308
; GENERAL INFORMATION:
;   APPLICANT: IIJIMA, Osamu
;   APPLICANT: GOTO, Takeshi
;   APPLICANT: SHIMADA,Takeshi
;   TITLE OF INVENTION: HIV Infection Inhibitors
; FILE REFERENCE:
;   CURRENT APPLICATION NUMBER: US/09/582,224A
;   CURRENT FILING DATE:  2000-07-21
;   PRIOR APPLICATION NUMBER: PCT/JP99/06534
;   PRIOR FILING DATE: 1999/11/24
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: Microsoft Word
; SEQ ID NO 5
;   LENGTH: 1664
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
; FEATURE:
;   OTHER INFORMATION: cDNA of CXCR4
US-09-582-224A-5

Query Match       50.7%;  Score 951.8;  DB 3;  Length 1664;
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Best Local Similarity   80.2%;   Pred. No. 3.3e-177;
Matches 1209;   Conservative   0;   Mismatches 252;   Indels 46;   Gaps 6;

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Qy    45  CAGGTGCAGGTAGCAGTGACCCTGTGAGGCGTTTGGTGCTCCGGTAACCACCACGGCTGT 104
          |||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db     1  CGGCAGCAGGTAGCAAGTGACGCCCGAGTGCGTCCAGTAGCCACCGCCACCGCATCTGG 60

Qy   105  AGAGCGAGTGTTGCCATGCAAGCCGATCAGTCGAGTATATACACTTCTGATAACTACTCT 164
          |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db    61  AGAACCAGCCGGTTACCATGGA------GGGGATCAGTATATACACTTCAGATAACTACACC 115

Qy   165  GAAGAAGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCCGGATGAAAAC 224
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   116  GAGGAAATGGGCTCAGGGGCTCAGTGACTATGACTCCATGAAGGAACCCTGTTTCCGTGAAGAAAAT 175

Qy   225  GTCCATTCAATAGGATCTTCCTGCCACCATCTACTTCATCATCTCTTGACTGGCATA 284
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   176  GCTAATTTCAATAAAATCTTCTGCGCCACCATTCTCCATCATCTTCTTAACTGGCATT 235

Qy   285  GTCGGCAATGAGATTGGTGATCCTGGTCATGGGTTACCAGAGAAGAAGCTAAGGAGCATGACG 344
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   236  GTGGGCAATGAGATTGGTCATCCTGGTCATGGGTTACCAGAGAAGAAACTGAGAAGCATGACG 295

Qy   345  GACAAGTACCGGCTGCACCTGTCAGTGGCTGACCTCCTTGTCATCACACTCCCCTTC 404
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   296  GACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCCTCTTTGTCATCACGCTTCCCTTC 355

Qy   405  TGGGCAGTTGATGGCCATGGCCATGGTACTTGGGAAATTTTGTGTAGGCTGTCCAT 464
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   356  TGGGCAGTTGATGGCCGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCAT 415

Qy   465  ATCATCTACACTGTCAACCTTACACGCACGGCTGTTCATCGCTTCATCCAGCTGCTGGAC 524
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   416  GTCATCTACACACAGTCCACACCTCTACAGCAGTGTCCTCATCCTGGCCTTCATCAGTCTGGAC 475

Qy   525  CGGTACCTGCCATTGTCCACGCCACCAACAGTCAAAGGCAAGGAAACTGCTGCTGAA 584
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   476  CGCTACCTGGCCATCGTCCACGCCACCAACAGTCAGAGGCCAAGGAAGCTGTTGGCTGAA 535

Qy   585  AAGGCAGTCTATGTGGGCGTCTGAATCCCAGCCCTCCTGACTATACCTGACTTCATC 644
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   536  AAGGTGGTCTATGTGGCGTCTGGATCCCTGCCCTGCTCCTGCTATTCCCGACTTCATC 595

Qy   645  TTTGCCGAGTCAGCCAGGGGACATCAGTCAGGGGGATGACAGAGGTACATCGTGACCGC 704
          ||||||||||                                          ||||||||||
Db   596  TTTGCCAACG-----------TCAGTGAGGCAGCAGATCAGATAGTATCGTGACCGC 640

Qy   705  CTTTACCCCGATAGCCGTGTGGATGGTGTTTTCAATTCAGCATATAATGTGGTCTC 764
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   641  TTCTACCCCCAATGACTTGTGGGTGGTGTGTTTCCAGTTTCAGCGTTTCAGCTTT 700

Qy   765  ATCCTGCCCGGCCATCGTCATCATCTCTCCTGTTACTTGCATCATCATCTTCAAGCTGTCACAC 824
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   701  ATCCTGCCCTGTATTGTCATCGTCTCTGTTATTGCATTATCATCTCCAAGCTGTCACAC 760

Qy   825  TCCAAGGGGCACCAGAAGCCGAAGGCCCTCAAGAACAGTCATCCTATCCTCCTAGCTTTC 884
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   761  TCCAAGGGGCACCACAGAGCGCAAGGCCCTCAAGACCACCAGTCATCCTCATCCCTGGCTTTC 820

Qy   885  TTTGCGCTGGCTGCTGCCATATTATGTGGGATCAGCATGCACTCCTTCATCCTTTTGGGA 944
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   821  TTCGGCTGTTGGCTGCTCTTACTACATTGGGATCAGCATGGACTGACTCCTTCATCCTCTGGAA 880

Qy   945  GTCATCAAGCAAGGATGTGACTTGCACAAGCCATTGTGCACAAGTGGATCTCCATCACACAGAG 1004
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   881  ATCATCAAGCACAGAGGGTGTGATGTTTGAGAGCTGCACACTGTGCACACTTTCCATCACCGAG 940

Qy  1005  GCCCTCGCCTTCTTCCACTGTTGCCTGAACCCCCATCCTCTATGCCTTCCTCGGGGCCAAG 1064
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    941  GCCCTAGCTTTTCTTCCACTGTTGTCTGAACCCCATCCTCTATGCTTCTTCCTTGGAGCCAAA 1000

Qy  1065  TTCAAAAGCTCTGCCCCAGCAGCTCGCCAACTCACCTGTGAGCGAGAGCCTCCAGCCTCAAGATC 1124
          |||||||||||||||||||||||||||||| |||||||||||||||
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Db  1001  TTTAAAACCTCTGCCCAGCACGCACTCACCTCTGTGAGCGAGAGGGTCCAGCCTCAAGATC 1060

Qy  1125  CTTTCCAAAGGAAAGGCGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGAATCCTCCAGT 1184
          ||||||||||||||||||||||||||||||  |||||  |||||||||||||||||||
Db  1061  CTCTCCAAAGGAAAGGCGAGGTGGACATTCATCGTGTTCCACTGAGTCTGAGTCTTCAAGT 1120

Qy  1185  TTTCACTCCAGCTAACCCTTATGCAAAGACTTATATAATATATATATATATGATAAAG 1244
          ||||||||||||||||||||||||||||||||  ||||||------TTTATACGATAAATAA 1172
Db  1121  TTTCACTCCAGCTAACACAGATGTAAAAGACTTTTT------TTTATACGATAAATAA

Qy  1245  AACTTTTTATGTTACACATTTCAGATATAAAGAGACTGACCCAGTCTTGTACAGTTTTT 1304
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1173  CTTTTTTTTAAGTTACACATTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTTT 1232

Qy  1305  TTTTTTTTTAATTGACTGTTGGGAGTTTATGTTCCTCTAGTTTTTGTGAGGTTTGACTT 1364
          ||||||||||                   |    |||||||||||   ||||  |||||
Db  1233  ATTGCTTGTTGGATTTTTGT-----CTTGTGTTTCTTTAGTTTTTGTGAAGTTTAATTG 1286

Qy  1365  AATTTATATAAATATATGTTTTTGTTTGTTCATGTGAATGAGCGTCTAGGCAGGACCTG 1424
          |||||||||     |||||||||||     |||||||||||||||||||||||||||||||
Db  1287  ACTTATTTATA----TAAATTTTTTGTTTTCATATGATGTGTGTCTAGGCAGGACCTG 1342

Qy  1425  TGGCCAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTAGAACTGTAGAGGAAGAA 1484
          |||||||||||||||||||||||||||||||||||||||||||        |||||||
Db  1343  TGGCCAAGTTCTTAGTTGCTGTATGGTCTCGTGGTAGGACTGTAGAA-------AGGGA 1394

Qy  1485  ACTGAACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTTG 1544
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1395  ACTGAACATTCCAGAGCGTGTAGTTAATCACGTAAAGCTAGAAAATGATCCCCAGCTGTTT 1454

Qy  1545  CTGCATA 1551
          |||||||
Db  1455  ATGCATA 1461
```

RESULT 13
US-09-023-655-1213
; Sequence 1213, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
;; APPLICANT: Cocks, Benjamin G.
;; APPLICANT: Susan G. Stuart
;; APPLICANT: Jeffrey J. Seilhamer
;; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
;; TITLE OF INVENTION: EXPRESSION
;; NUMBER OF SEQUENCES: 1508
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 PORTER DRIVE
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/023,655
;; FILING DATE: HEREWITH
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Zeller, Karen J.
;; REGISTRATION NUMBER: 37,071
;; REFERENCE/DOCKET NUMBER: PA-0001 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166

```
;
;  INFORMATION FOR SEQ ID NO: 1213:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH:   1664 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;     LIBRARY:  GENBANK
;     CLONE:  g219868
US-09-023-655-1213

Query Match      50.7%;  Score 951.8;  DB 3;  Length 1664;
Best Local Similarity   80.2%;  Pred. No. 3.3e-177;
Matches 1209;  Conservative  0;  Mismatches 252;  Indels 46;  Gaps 6;
```

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Qy    45  CAGTGCAGGTAGCAGTGACCCTGTTGGTGTCCGTAACCACCACGGCTGT  104
              ||| ||||  ||| |  || ||  | ||  | |||||| ||||  |||
Db     1  CGGCAGCAGGTAGCAAAGTGACGCCGAGGGCCTCCAGTGCTCCACCGCCATCTGG   60

Qy   105  AGAGGCGAGTGTTGCCATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTCT  164
               |||||    ||   |||     ||||  ||||| || |||| ||| ||||||||||
Db    61  AGAACCAGGCGGTTACCATGA-----GGGGATCAGTATATACACTTCAGATAACTACACC  115

Qy   165  GAAGAAGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAAC  224
              || |  ||| |  ||||||||||||||||| ||| ||||| |||||||| |||||| |||
Db   116  GAGGAAATGGGGCTCAGGGGACTATGACTCCATGAAGAACCCTGTTTCCGTGATGAAGAAAT  175

Qy   225  GTCCATTTCAATAGGATCTTCCTGCCCACCATCTCACTTCATCATCTTCTGACTGGCATA  284
              |||| ||||||||||    ||||||||||||  ||||||  |||  ||| ||||||||
Db   176  GCTAATTTCAATAAAATCTTCCTGCCCACCATCATCCATCATCTTCTTCTTAACTGGCATT  235

Qy   285  GTCGGCAATGGATGGTGATCCTGTCATGGGTTACCAGAAGAAGCTAAGGAGCCATGACG  344
              || |||||||| |||||||||| |||||| ||||||||||||||||| |||||||||||
Db   236  GTGGGCAATGGATTGGTCATCCTGTCATGGGTTACCAGAAGAAGCTGAGAAGCCATGACG  295

Qy   345  GACAAGTACCGGCTGCACCTGTCAGTGCTGGCTGCACTTTGTCATCACACACTCCCCCTTC  404
              |||||||||||||||||||| |||||||||| ||||| |  ||||  ||||||||| |||
Db   296  GACAAGTACAGGCTGCACCTGTCAGTGCTGGCCGCACCTCCTTTGTCATCACGCGTTCCCCTTC  355

Qy   405  TGGGCAGTTGATGCCATGGCCGTGGCAAACTGGTACTTTGGGAAATTTTGTGTTAAGGCTGTCCAT  464
              ||||||||||||||| ||||||  ||||||||||  ||| ||||   || ||||  ||||| ||||
Db   356  TGGGCAGTTGATGCCGTGGCCGTGGCAAACTGGTACTTTTGGGAAACTTCCTATGGCAAGGCAGTCCAT  415

Qy   465  ATCATCTACACTGTCAACCTTCTACAGCAGCCGTTCCATCCTGGCCTTCATCAGCCTGGAC  524
              ||||| ||||||  ||| ||| |||||||||| |||||  |||||||||||||||||||||
Db   416  GTCATCTACAGTGTCAACCTTCTACAGCAGCGTGTCCCTTCATCCTGGCCTTCATCAGTCTGGAC  475

Qy   525  CGGTACCTTCGCCATTGTCCACGCCACCACCAACAGTCAAAGGCCACCAGAAACTGCTGGCTGAA  584
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Db   476  CGCTACCTGGCCATCGTCCACGCCACCACCAACAGTCAGAGGCCAAGGAAGCTGTTGGCTGAA  535

Qy   585  AAGGCAGTCTATGTGGGCGTCTCGATCCTCCTCCCTGACTATACCTGACTTCATC  644
              ||||| |||| ||||||||| ||||||||||||||||| ||||||||||||||||
Db   536  AAGGTGGTCTATGTTGGGCGTCTGGATCCTCGTGCTGCTCGTGATCGTGACTTCATC  595

Qy   645  TTTGCCGACGTCAGCCAGCGGACATCAGTCAGGGGGATGACAGGTACATCTGTGACCGC  704
              |||||  ||||||||   |||||||||||||  || |||||||||  || |||||||||
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Qy   705  CTTTACCCCGATAGCCTGTGGATGATGGTGTGTGTTTCAATTCAGATCAGTTATATAGTGGGTCTC  764
              |||| ||||||| |||||| ||||||||| | |||||||||| ||||| ||||||||||||||
Db   641  TTCTACCCCAATGACTTGTGGGGTTGTGTTCAGTTTTATCATTATCATCATGTGGCCTT  700

Qy   765  ATCCTGCCCGGCATCGTCATCCTCTCGTACTGCATCATCTTCTAAGCTGTCACAC  824
              ||||||  |||||| | ||||||||||| |  || |||||||||||| || ||||
Db   701  ATCCTGCCTGGTATTGTCATCATCTCCTGTGCTATTATCATCTCCGACTTCATC  760

Qy   825  TCCAAGGGCCACCAGAAGCGCAAGGCCCTCAAGACGACACAGTCATCCTCCATCCTAGCTTTC  884
              ||||| ||||||||||||||||||||||| |||| ||||||||||||||||||||| |||||
Db   761  TCCAAGGGCCACCAGAAGCGCAAGGCCCTCAAGACGACACACAGTCATCATCCTCTGCTTTC  820

Qy   885  TTTGCCTGCTGGCTGCCATATTATGTGGGGATCAGCAGCATCGATGCACTCCTTTTTGGGA  944
              |||||||||| |  ||||||||||||||||||||| ||||||||| |  ||||||||| |||
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Db   821  TTCGCCTGTGGCTGCCTTACTACATGGGATCAGCATCAGCTGCCTTTCATCCTCCTGGAA  880

Qy   945  GTCATCAAGGATGACTGACTTCGAGAGCAGCATTGTGCACAAGTCGACATCCATCACAGAG  1004
              |||||||||||| |||||||   |||| |  || ||||||| |||||||||||||||||||
Db   881  ATCATCAAGGCAAGTGTGAGTTTGAGACACTGTTGAGAACACTGGCAAGTGGATTTCCATCACCGAG  940

Qy  1005  GCCCTGCCTTCTTCCACTGTTGCCTGAACCCATCCTCATGCCTTCCTCCTCGGGGGCCAAG  1064
              |||||||| ||||||||| || |||||  | |||||| |||||||||| |||| |||||||
Db   941  GCCCTAGCTTCTTCCACTGTTGTCTGAACCCCATCCTCATGCTTTCCTTCCTTGGGAGCCAAA  1000

Qy  1065  TTCAAAGTCTCTGCCCAGCATGCACTCAACTCCATGAGCAGGAGGCTCCAGCCTCAAGATC  1124
              || ||| | |||||||| | ||  |||| || ||| |||| ||||| ||||||||||||||
Db  1001  TTTAAAACCTCTGCCCAGGACGCGCTCAACTCTCCGTGAGCAGAGAGGGTCCAGCCTCAAGATC  1060

Qy  1125  CTTTCCAAAGGAAAGCGGGTGGACACTCTTCCGTTCCTCCTCCACGGAGTCAGGAATCCTCCAGT  1184
              || ||||||||||||| ||| | ||| ||   | ||||  | ||| |||||  |||||  ||||
Db  1061  CTCTCCAAAGGAAAGCGAGGTGGACAATTCATCATCTGTTTCCACTGAGTCTTGAGTCTTCAAGT  1120

Qy  1185  TTTCACTCCAGCTAACCCTATGCAAAGACTTATATATACATTTTTT------TTTATACGATAAATAA  1244
              ||||| ||||||| ||  ||||| | ||| |||||| ||| |||      ||  | ||||  ||
Db  1121  TTTCACTCCAGCTAACACAGAGAACAGAGACTTTTT------TTTATACGATAAATAA  1172

Qy  1245  AACTTTTTTATGTTACACATTTTCCAGATATAGAGACTGACCAGTCTTGTACAGTTTTT  1304
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Db  1173  CTTTTTTTAAGTTACACATTTTTCAGATATAAAGAGACTGACCAATATTGTACAGTTTTT  1232

Qy  1305  TTTTTTTTTTTTAATTGACTGTTGGGAGTTTATGTTCCTCTAGTTTTTGTTGTGAGGTTTGACTT  1364
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Qy  1365  AATTTATATAAATAYTGTTTTTTGTTGTTTCATGTGAATGAGACGCTCAGGCAGGACCTG  1424
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Db  1287  ACTTATTTATA------TAAATTTTTTGTTTTTGTTTCATATTGATGTGTCTCGGGTAGGACTGAGA  1342

Qy  1425  TGGGCCAAGTTCTTAGTAGCTGTTTTATCTGTGTGGAGGACTGTAGAGAGGAAGAA  1484
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Db  1343  TGGGCCAAGTTCTTAGTTGCTGTTATGTCTGTGTATGTCTCGGGTAGGACTGTAGAA-------AAGGGA  1394

Qy  1485  ACTGAACATTCCAGAAATGTGTGTAAATTGAATAAAAGCTAGCCGTGATCCTGATCCGTGTTG  1544
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Qy  1545  CTGCATA  1551
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RESULT 14
US-09-016-434-1235
; Sequence 1235, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
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PRIOR APPLICATION DATA:
  APPLICATION NUMBER:
  FILING DATE:
  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
  NAME: Zeller, Karen J.
  REGISTRATION NUMBER: 37,071
  REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (650) 855-0555
  TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1235:
SEQUENCE CHARACTERISTICS:
  LENGTH: 1225 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
IMMEDIATE SOURCE:
  LIBRARY: GENBANK
  CLONE: g189313
US-09-016-434-1235

Query Match   45.8%;   Score 859;   DB 3;   Length 1225;
Best Local Similarity   83.3%;   Pred. No. 4.6e-159;
Matches 1009;   Conservative   0;   Mismatches 180;   Indels 22;   Gaps 2;

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Qy  136 TGAGTATATACACTTCTGATAACTACTTCTGAAGAAGTGGGGTCTGGAGACTATGACTCCA 195
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Qy  196 ACAAGGAACCCTGCTTCCGGGATGAAAACGTCATTCAATAGGATCTTCCTGCCCACCA 255
             ||||||||||||||||||   |||||||||||  |||||||||||||||||||||||
Db   96 TGAAGGAACCCTGTTCCGTGAAGAAAATCTTTCAATAAAATCTTCCTGCCCACCA 155

Qy  256 TCTACTTCATCATCTTCTTGACTGGCATAGTCGGCAATGATTGGTGATCCTGGTCATGG 315
            ||||||||||||||||||||||    |||||| |||||||||||||||||||||||||
Db  156 TCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATGG 215

Qy  316 GTTACCAGAAGAAGTAAGGAGACATGACGGACAAGTACCGGCTCAGTGGCTG 375
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Db  216 GTTACCAGAAGAAACTGAGAAGAACATGAGCAGCAGTACACGGCTCAGTGGCCG 275

Qy  376 ACCTCCTCTTGTCATCACACTCCCCTTCTGGGCCAGTGATGCCATGGCCATGGTGACTGGTACT 435
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Db  276 ACCTCCTCTTTGTCATCACAGCTTCCCTTCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACT 335

Qy  436 TTGGGAAATTTTTCTGTGTAAGGCTGTCCATATCATCTACACTGTCAACCTTCACAGCAGCG 495
            |||||||        ||||||||||| |||||||||||||||||||||  ||||||||||||
Db  336 TTGGGAACTTCCCATGCAAGGCAGTCCATGTCATCATCCTACAGCAGTTCAACCTTCACAGCAGTG 395

Qy  496 TTCTCATCCTGGCCTTCATCAGCCTGGACGCGGTACCTCGCCATTGTCACGCCACCAACA 555
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Qy  556 GTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTGTCATGTGGCGTCTGAATCCCAG 615
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Db  456 GTCAGAGGCCAAGGAAGCTTGGCTGAAAAGGTGGTCATGTTGGCCGTCTGATCCCCTG 515

Qy  616 CCCTCCCTCCTGACTACCTGACTTCATCTTTGCCAGCTAGCTCAGCCAGGGGGACATCAGTC 675
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Db  516 CCCTCCCTGCTGACTATTCCCGACTTTCATCCTTGCCAACG--------TCAGTG 560

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            |||||||||||||||||||||| ||||||||||||||||  |||||||||||||| |||||
Db  561 AGGCAGATGACAGATATCGTGACCGGCCTTCTACCCCCAATGACTTGTGGGTCGTTGTGT 620

Qy  736 TTCAATTCCAGCATATAATGGTGGGTCTCATCCTCGCCGCCATCGTCGTCCTCGTT 795
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Qy  796 ACTGCATCATCATCTTCAAGCTGTCACACTCCAAGGGCCACCAGAAGAAGCCAAGGCCCTCA 855
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Db  681 ATTGCATTATCATCATCTTCAAGCTGTCACACTCCACACTTCCAAGAAGGGCCACCAGAAGCGCCAAGAGCCCCTCA 740

Qy  856 AGACGACAGTCATCCTCATCCTTCAGCTTTTCTTGCCGCTGCGCTGCCATATTATGTGGGGA 915
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Db  741 AGACCACAGTCATCCTCATCCTCGGCTTTTTCTTCTGGGCCTTGCCTTACTACACATTGGGA 800

Qy  916 TCAGCATCGACTCCTTCATCCTTTTGGGGAGTCATCAAGCAGGATGTGACTTCGAGAGCA 975
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Db  801 TCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAGGTGTGAGTTTGAGAACA 860

Qy  976 TTGTGCACAAGTGGATCTCCATCACAGAGAGCCCCTGCCTTCTCCACTGTTGCCTGAACC 1035
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Db  861 CTGTGCACAAGTGGGATTTCCATCACCGAGGCCCCTAGCTTTCTTCCACTGTGTCTGAACC 920

Qy 1036 CCATCCTCTATGCCTTCCTGGGGCAGGGTCCAAGTTCAAAAGCTGGCCCAGCATGCACTCAACT 1095
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Db  921 CCATCCTCTATGCTTTCCTGGGAGCCCAAATTTTAAAACCTCTGCCCAGCACGCACTCACCT 980

Qy 1096 CCATGCAGAGGCTCCAGCGTCGACGAATCCTCCCAGTTTCACTCCAGCTAACCCTTATGCAAAGACT 1155
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Db  981 CTGTGGAGCAGAGGGTCCAGCCTCCAGGATCCTCCAAGATTTTCACTCCAGCTAAGACAGATGTAAA---- 1040

Qy 1156 CCGTCTCCACGGAGTCAGAATCCTCCAGTTTCACTCCAGCTAACCCTTATGTTACACATTTTCCAGATACT 1215
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Db 1041 CTGTTTCCACTGACCTGAGTCTTCAAGTTTCACTCCAGCTAACACAGATGTAAA------- 1096

Qy 1216 TATATAATATATATATATATGATAAAGAGAACTTTTTTATGTTACACATTTTCCAGATAT 1275
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Db 1097 ---AGACTTTTTTTTTTATACGATAAAATAACTTTTTTTTAAGTTACACATTTTCAGATAT 1153

Qy 1276 AAGAGACTGACCAGTCTTGTACAGTTTTTTTTTTATTTTTTATTGACTGTTGGGAGTTTAT 1335
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Db 1154 AAAAGACTGACCAATATTGTACAGTTTTACAGTTTTATTGCTTGTGCTGGATTTTGTCTTGTGTTTCT 1213

Qy 1336 GTTCCTCTAGT 1346
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Db 1214 TTAGTTTTTGT 1224
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RESULT 15
US-08-153-848-45
; Sequence 45, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.
; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:

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;   TELEPHONE:   (312) 474-6300
;   TELEFAX:     (312) 474-0448
;   TELEX:       25-3856
; INFORMATION FOR SEQ ID NO:  45:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:   1317 base pairs
;     TYPE:     nucleic acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA
;   FEATURE:
;     NAME/KEY:  CDS
;     LOCATION:  201..1211
US-08-153-848-45
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Query Match         44.5%;   Score 834.6;  DB 2;   Length 1317;
Best Local Similarity  83.9%;   Pred. No. 2.8e-154;
Matches  977;  Conservative  0;  Mismatches  164;  Indels  24;  Gaps  2;

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Qy    434  CTTTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTACACTGTCAACCTCTACAGCAG  493
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Qy    914  GATCAGCATCGACTCCTTCATCCTTTGGGAGTCATCAAGCAAGGATGCATCAAGCTTCGAGAG  973
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Db    929  GATCAGCATCGACTCCTTCATCCTCTGGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAA  988

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Db   1227  ------------AGACTTTTTTTATACGATAAATAACCTTTTTTTTTAAGTTACACATTTTTCAGAT  1279

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Search completed: January 10, 2006, 20:53:55
Job time : 411 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 20:34:06 ; Search time 1633 Seconds
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Title: US-09-367-052-1
Perfect score: 1877
Sequence: 1 ccatcctaatacgactcact........aaaaaaaaaaaaaaaaaa 1877

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413469005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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              7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
              8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
              9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
             10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1758	93.7	1758	8	US-10-785-230-4	Sequence 4, Appli
2	974.4	51.9	1737	3	US-09-104-063-3	Sequence 3, Appli
3	974.4	51.9	1737	7	US-10-666-689-5	Sequence 3, Appli
4	970	51.7	1826	8	US-10-723-860-5773	Sequence 5773, Ap
5	964.2	51.4	1699	8	US-10-775-920-373	Sequence 373, App
6	960.4	51.2	1662	5	US-10-706-265-11	Sequence 11, Appl
7	952.8	50.8	1679	5	US-10-151-274-14	Sequence 14, Appl
8	952.8	50.8	1679	5	US-10-025-567A-75	Sequence 75, Appl
9	952.8	50.8	1679	6	US-10-021-660-58	Sequence 58, Appl
10	952.8	50.8	1679	6	US-10-170-385-332	Sequence 332, App
11	952.8	50.8	1679	6	US-10-341-434-177	Sequence 177, App
12	952.8	50.8	1679	7	US-10-172-118-912	Sequence 912, App
13	952.8	50.8	1679	7	US-10-211-462-80	Sequence 80, Appl
14	952.8	50.8	1679	7	US-10-181-906-9	Sequence 9, Appli
15	952.8	50.8	1679	7	US-10-342-887-912	Sequence 912, App
16	952.8	50.8	1679	8	US-10-775-920-366	Sequence 366, App
17	952.8	50.8	1679	8	US-10-278-698-64	Sequence 64, Appl
18	952.8	50.8	1679	8	US-10-278-698-578	Sequence 578, App
19	952.8	50.8	1679	9	US-10-888-313A-62	Sequence 62, Appl
20	952.8	50.8	1679	9	US-10-486-471-19	Sequence 19, Appl
21	952.8	50.8	1711	3	US-09-971-392-20	Sequence 20, Appl
22	952.8	50.8	1711	6	US-10-101-510-459	Sequence 459, App
23	951.8	50.7	1664	7	US-10-641-643-1213	Sequence 1213, Ap
24	951.8	50.7	1664	8	US-10-775-920-369	Sequence 369, App
25	947.6	50.5	1645	8	US-10-775-920-374	Sequence 374, App
26	947.6	50.5	1645	9	US-10-505-680-185	Sequence 185, App
27	944.8	50.3	1670	3	US-09-880-107-2143	Sequence 2143, Ap
28	944.8	50.3	1670	6	US-09-960-706-636	Sequence 636, App
29	944.8	50.3	1670	6	US-10-372-683-1	Sequence 1, Appli
30	944.8	50.3	1670	7	US-10-440-464-77	Sequence 77, Appl
31	944.8	50.3	1670	8	US-10-717-597-317	Sequence 317, App
32	944.8	50.3	1670	8	US-10-775-920-367	Sequence 367, App
33	938.2	50.0	1950	8	US-10-775-920-368	Sequence 368, App
34	938.2	50.0	1950	8	US-10-723-860-1279	Sequence 1279, Ap
35	936.8	49.9	1588	8	US-10-785-230-2	Sequence 2, Appli
36	934.4	49.8	1637	6	US-10-160-401-1	Sequence 1, Appli
37	921.2	49.1	1050	9	US-10-775-920-372	Sequence 372, App
38	905.6	48.2	1225	6	US-10-486-706-54	Sequence 54, Appl
39	859	45.8	1225	6	US-10-101-510-741	Sequence 741, App
40	859	45.8	1225	8	US-10-305-720-1235	Sequence 1235, Ap
41	859	45.8	1224	8	US-10-775-920-370	Sequence 370, App
42	847	45.1	1059	6	US-10-101-510-674	Sequence 674, App
43	809.6	43.1	1059	6	US-09-813-651B-84	Sequence 84, Appl
44	809.6	43.1	1059	6	US-10-014-322A-125	Sequence 125, App
45	809.6	43.1		6	US-10-160-401-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-785-230-4
; Sequence 4, Application US/10785230
; Publication No. US2004020937A1
; GENERAL INFORMATION:
; APPLICANT: KISHIMOTO, Tadamitsu
; APPLICANT: NAGASAWA, Takashi
; APPLICANT: TACHIBANA, Kazunobu
; APPLICANT: CHUGAI SEIYAKU KABUSIKI KAISHA
; TITLE OF INVENTION: Vascularization Inhibitors
; FILE REFERENCE: 46124-5042-US
; CURRENT APPLICATION NUMBER: US/10/785,230
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: PCT/JP99/01448
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: JP10/95448
; PRIOR FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Mus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1080)
; OTHER INFORMATION:
US-10-785-230-4

Query Match   93.7%; Score 1758; DB 8; Length 1758;
Best Local Similarity   100.0%; Pred. No. 0;
Matches 1758; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   120 ATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTTCTGAAGAAGTGGGGTCT 179
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Db   1 ATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTTCTGAAGAAGTGGGGTCT 60

Qy   180 GGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAACGTCCATTTCAATAGG 239
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Qy   300 GTGATCCTGGTCATGGGTTACCAGAAGAAGCTAAGGAGCATGACCGGACAAGTACCGGCTG 359
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Db 181 GTGATCCTGGTCATGGGTTACCAGAGAAGAGCTAAGGAGCATGACGGACAAGTACCGGCTG 240

Qy 360 CACCTGTCAGTGGCTGGCTGACCTCCCTTTGTCATCACACACTCCCTTCTGGGCAGTTGATGCC 419
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Qy 420 ATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTACACTGTC 479
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Db 301 ATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTACACTGTC 360

Qy 480 AACCTCTACAGACAGCAGCGTTCTCATCCTGCCTTCATCAGCCTGACCGGTACCTCGCCATT 539
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Db 361 AACCTCTACAGACAGCAGCGTTCTCATCCTGCCTTCATCAGCCTGACCGGTACCTCGCCATT 420

Qy 540 GTCCACGGCCACCAACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTG 599
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Qy 600 GGGCTCTGGATCCCAGCCCTCCTGACTATACCTTTGCCGACGTCAGC 659
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Qy 660 CAGGGGGACATCAGTCAGGGGATGACACAGGTACATCTGTGACCGGCCTTTACCCCGATAGC 719
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Qy 900 CCATATTATGTGGGGATCAGCATCGACTCCTTCATCCTTTGGGAGTCATCAAGCAAGGA 959
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Qy 960 TGTGACTTCGACAGTGCACAAGTGATCTCCATCACAGAGAGCCCTGCCTTCTTC 1019
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Db 901 CACTGTTGCCTGAACACCCCATCCTCTATGCCTTCCTCGGGCCAAGTTCAAAAGCTCTGCC 960

Qy 1080 CAGCATGCACTCAACTCAACTCCATGAGCAGAGAGCCTCCAGCTCCAAGATCCTTTCCAAGAGGAAAG 1139
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Db 961 CAGCATGCACTCAACTCAACTCCATGAGCAGAGAGCCTCCAGCTCCAAGATCCTTTCCAAGAGGAAAG 1020

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Db 1021 CGGGGTGGACACTCTTCCGTCCACGGAGTCAGAATCCTCCAGTTTTCACTCCAGCTAA 1080

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Qy 1320 ACTGTTGGGAGTTTATGTTCCTCTAGTTTTTGTGAGGTTTGACTTAATTTATATAAATAT 1379
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Db 1201 ACTGTTGGGAGTTTATGTTCCTCTAGTTTTTGTGAGGTTTGACTTAATTTATATAAATAT 1260

Qy 1380 TGTTTTTTTGTTTGTTTCATGTGAATGAGTGAATGAGGTCTAGGCACGGACCCTGTGGCCAAGTTCTTAG 1439
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Db 1261 TGTTTTTTTGTTTGTTTCATGTGAATGAGTGAATGAGGTCTAGGCACGGACCCTGTGGCCAAGTTCTTAG 1320

Qy 1440 TAGCTGTTTTATCTGTGTGTAGGACTGTAGAACTGTGAGAGAAGAGGAAGAAACTGAACATTCCAGA 1499
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Db 1561 AAGATGGCACTTAAAACCAAAGCCTGAAATGGTGGTAGAAAATGCTGGGGTTTTTTTGTT 1620

Qy 1740 TGTTTGTTTTTCAGTTTTCAAGAGTAGATTGACTTCAGTCCCTACAAATGTACAGTCTT 1799
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Qy 1860 AAAAAAAAAAAAAAAA 1877
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Db 1741 AAAAAAAAAAAAAAAA 1758

RESULT 2
US-09-104-063-3
; Sequence 3, Application US/09104063
; Patent No. US2002016835A1
; GENERAL INFORMATION:
;   APPLICANT: Lee, James
;   APPLICANT: Wood, William I.
;   TITLE OF INVENTION: PF4A Receptors
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/104,063
;   FILING DATE: 24-June-1998
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/701265
;   FILING DATE: 22-AUG-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/664228
;   FILING DATE: 06-JUN-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/076093
;   FILING DATE: 11-JUN-1993
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/810782
;   FILING DATE: 19-DEC-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Love, Richard B.

```
;   REGISTRATION NUMBER: 34,659
;   REFERENCE/DOCKET NUMBER: P0706P2C2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415/225-5530
;   TELEFAX: 415/952-9881
;   TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1737 base pairs
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
US-09-104-063-3

Query Match      51.9%;   Score 974.4;  DB 3;  Length 1737;
Best Local Similarity   76.1%;   Pred. No. 3.4e-211;
Matches 1391;  Conservative  0;  Mismatches 301;  Indels 136;  Gaps 10;
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Db   80 CAGCGGGGTTACCATGA------GGGGATCAGTATATACACTTCAGATAACTACACCGAGGA   134

Qy   170 AGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAACGTCCA   229
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Db   135 AATGGGCTCAGGGGACTATGACTCCATGAAGGAACCCTGTTTCCGTGAGAAAAATGCTAA   194

Qy   230 TTTCAATAGGATCTTCCTGCCCACCATCTACTTCATCATCTTCTGACTGGCATAGTCGG   289
           |||||||| | | ||||||||||||||| ||||||||||||||||| || | ||||| |
Db   195 TTTCAATAAAATCTTCCTGCCCACCATCTACTTCATCATCTTCTAACTGGCATGTGTGGG   254

Qy   290 CAATGGATTGGTGATCCTGTCATGGTACCAGGAGAAGCTAAGGAGCATGACGGACAA   349
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Db   315 GTACAGGCTGCACCTGTCAGTGGCGACCTCTCTTTGTCATCACGCTTCCCTTCCTCGGGC   374

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Db   435 CTACACAGTCAACCTCTACAGACGCGTCCTCATCCTGGCCTTCATCAGCCTGGACCGCTA   494

Qy   530 CCTCGCCATTGTCACGCCACCACCACAGCTCAAGGCCAAGGAAACTGCTGGCTGAAAAGGC   589
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Db   495 CCTGGCCATCGTCACGCCACCACCACAGCTCAGAGGCCAAGGAGCTGTTGGCTGAAAAGGT   554

Qy   590 AGTCTATGTGGGGCGTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTTGC   649
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Db   555 GGTCTATGTTGGGCGTCTGGATCCTGACTATTCCCGACCTATTCCCGACTTCATCTTTGC   614

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Db   615 CAACG--------TCAGTGAGGCAGATGACAGTACATCTGTGACCGGCCGCTTCTA   659

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Db   660 CCCCAATAGCACTTCTGGGTTTGTGTTCCAGTTTCAGCACACATTGGTTGGCCTTATCCT   719

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Db   720 GCCTGGTATTGTCATCCTCTCTGCATTATCATCATCTTCCCAAGCTGTCACACTTCCCA   779

Qy   830 GGGCACCAGAAGCCAAGGCCCTCAAGACGCCCTCAAGACGA   889
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Db   840 CTGTTGGCTGCCTTACACATTGGGAT CAGGATCAGCATCAGCGACTGACTCCTTCATCCTTCCTGGAAATCAT   899

Qy   950 CAAGCAAGGATGTGACTTGACTTGCACAAGTGGATCTCCATCAAGAGGGCCCT   1009
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Qy   1130 CAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCACGAGCTGAGAATCCTCCAGTTTTCA   1189
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Db   1080 CAAAGGAAAGCGAGGTGGACATTCATCATCTCGTGAGTCTGAGTCTCGAGTCTTCAAGTTTTCA   1139

Qy   1190 CTCCAGCTAACCCCTATGCAAAGACTTATATATATATATATAGAACTT   1249
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Db   1140 CTCCAGCTAA------CACAGATGTAAAAGACTTTTTTTTATACGATAAATAACTTTT   1191

Qy   1250 TTTTATGTTACACATTTCAGATAATAAGAGACTGACCAGTCTGTACAGTTTTTTTTTT   1309
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Db   1192 TTTAAGTTACACATTTTCAGATATAAAAGACTGACCAATATTGACAGTTTTTATTGC   1251

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Qy   1430 AAGTCTTAGTAGCTGTTTATCGTGTGTAGGACTGTAGAGGAGAAACTGA   1489
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Db   1362 AAGTCTTAGTTGCTGTATGTCTCGTGGTAGGACTGTAGAA--------AAGGGAACTGA   1413

Qy   1490 ACATTCCAGAATGTGTGAAATTTGTGTAAGGCTGTCCATATCACTTCCTCAGCTGTCTGCA   1549
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Qy   1550 TAATCTCTCATTCCGAGGAGCAGCACCCCACCCCCCCACCCCCCATTCTTAAAT   1609
           || | | ||| |
Db   1474 TAGATAATCTCTCCA------------AGGGAACTGA   1488

Qy   1610 TGTTTGGTTATGCTGGTGATGGTTGTTTGTGTTTTTTGTTGTTGTTTTTTT   1669
           ||||| || ||||| |||| |||| | | | |||| |||| || ||||
Db   1489 ---------------------TTCCCGTGGAACGTTTTTCCCGTGTTCTTAAGACGTGAT   1525

Qy   1670 TTTTCTGTAAAGATGGCACTTAAAACCAAAGCCTGAAATGGTGTGGTAGAAATGCTCGGGGT   1729
           ||| || ||||| ||||| |||||||| ||| | |||| ||| || | ||| |||
Db   1526 TTTGGCTGTAGAAGATGGCACTTATTAAAACCAAAGTGGT-ATAGAAATGCTCG---   1581

Qy   1730 TTTTTTTGTTGTTGTTTTTTCAGTTTTCAGTTTCAGACTTCCTACACAAAT   1789
           ||||| |||| || |||||| ||||||||| ||||||||||
Db   1582 ---------------TTTTTCAGTTTTCAGTTTCAGACTTCCTACACCTAC-AGT   1623

Qy   1790 GTACAGTCTTGTATTACATTGTTAATAAAGTCAATGATAAAACTTAAAAAAAAAAAAA   1849
           |||||||| ||| |||||| |||| || | || ||||| | ||| |||||||||||||||
Db   1624 GTACAGTCTTGTATTAAGTTGTTAATAAAAGTACATGTTAAACTTAAAACTTAAAAAAAAAAAAA   1683

Qy   1850 AAAAAAAAAAAAAAAAAAAAAAAAAAA   1877
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Db   1684 AAAAAAAAAAAAAAAAAAAAAAAAAAAA   1711

RESULT 3
US-10-666-689-3
; Sequence 3, Application US/10666689
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; Publication No. US2004003783OA1
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Human PF4A Receptors, Nucleic Acid Encoding and
; TITLE OF INVENTION: Antibodies Binding Thereto
; FILE REFERENCE: P0706P2C2D2C1
; CURRENT APPLICATION NUMBER: US/10/666,689
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 09/104,063
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: US 08/701,265
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/664,228
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/076,093
; PRIOR FILING DATE: 1993-06-11
; PRIOR APPLICATION NUMBER: US 07/810,782
; PRIOR FILING DATE: 1991-12-19
; PRIOR APPLICATION NUMBER: US 07/677,211
; PRIOR FILING DATE: 1991-03-29
; NUMBER OF SEQ ID NOS: 6
;
; SEQ ID NO 3
;   LENGTH: 1737
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-10-666-689-3

Query Match      51.9%;  Score 974.4;  DB 7;   Length 1737;
Best Local Similarity   76.1%;  Pred. No. 3.4e-211;
Matches 1391;  Conservative   0;  Mismatches 301;  Indels 136;  Gaps   10;
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Qy     50 GCAGGTAGCAGTGACCCTTGAGGCGTTTGGTGTGCTCCGGTAACCACCACCACGGCTGTAGAGC 109
          || ||||  ||  ||||||||||| |||||||| || ||||||||||| |||||||||||||
Db     20 GCGCGGCGCAAAGTGACGCCGCAGGGCCTGAGTGCTCAGTGAGCCACCGCATCTGGAGAAC 79

Qy    110 GAGTGTTGCCATGAACCAGTCAGTGTGAGTATATACAAAGACTTCTGATAACTACTCTGAAGA 169
          |||||||| |  || |||||||||||||||||||||   |||||||||||||||||
Db     80 CAGCGGGTTACCATGGA------GGGGATCAGTAGTACACAGATAATAACTACCGAGGA 134

Qy    170 AGTGGGGGTCTGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAACGTCCA 229
          |||||||||||||||||||||||| || |||||||||||||||||||||||||||||
Db    135 AATGGGGCTCAGGGGACTATGACTCCATGAGGAGAACCCTGTTTCCGTGAAGAAAAATGCTAA 194

Qy    230 TTTCAATAGGATCTTCCTGCCCACCACTCACTTGTGGGAAATTTTTGTTGTAGGCTCATTGGCATAGGCATAGTCCG 289
          |||||||||||||||||||||||||||||||||||||| |  |||||||||||||||||||
Db    195 TTTCAATAAAATCTTCCTGCCCACCACTCACTCCATCATCCATCATCTTCTTAACTGACCGCATTGTGGG 254

Qy    290 CAATGGATTGGTGATCCTGTCATGGGTTACCAGAAGAGTCAAGGACATGAGGCACAA 349
          |||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||
Db    255 CAATGGATTGTCATCCTGGTTACCAGAAGAACTGAGAAGCATGACGACGACA 314

Qy    350 GTACCGGCTGCACCTGTCAGTGGTGGCCACCGCGCCACCGCTTCCCCTTCTGGGC 409
          |||||||||||||||||||||||||| |  ||||| ||||||||||||||||||
Db    315 GTACAGGCTGCACCTGTCAGTGGTGGCCGCCGCCACTCGATCCGCTTCCCCTTCTGGGC 374

Qy    410 AGTTGATGATGCCATGGCCATGGTACTTTGGGAAATTTTTGTTGTAAGGCTGTCCATATCAT 469
          ||||||| ||||| |||||| |||||||||||||||  | ||||||||||||||||||||
Db    375 AGTTGATGATGCCGTGGCAAACTGTACTTTGGGAACTTCCTGCAAGGAGTCCATGGCTCAT 434

Qy    470 CTACACTGTCAACCTCTACAGCAGCAGCGTTCTTCATCCTGGCCTTCATCAGTCTGGACCGGTA 529
          ||||||||||||||||||||||||||| ||||  ||||||||||||||||||||||||||||
Db    435 CTACACAGTCAACCTCTACAGCAGCAGCGTTCCTCCTGGCCTTCATCAGTCTGGACCGCTA 494

Qy    530 CCTCGCCATTGTCCACGCCACCAAACAGTCAAAGGCCAAGGAAACTGTGGCTGAAAAGGC 589
          |||||||||||||||| |||||||||||||||||||||| |||||||| ||||||||||
Db    495 CCTTGGCCATCGTCCACGCCACCAAACAGTCAGAGGCCAAGGAAGCTGTGTGGCTGAAAAGGT 554

Qy    590 AGTCTATGTGGGCGTCTGGATCCCAGCCCTCCTCCAGCCCCTCCTGTGCTACTACCTGACTTCATCTTTGC 649
          ||||||||||||||||||||||||||||| |||| || |||| | |||||||| ||||||||||||
Db    555 GGTCTATGTTGGCGTCTGGATCCCTGGATCCCTGCTGCTATTCCCGACTTCCCGACTTCATCTTTGC 614

Qy    650 CGACGTCAGCCAGGGGACGACATCAGTCAGGCGGGGATGACAGCAGTGACAGTAGCATCTGTGACCGGCCTTTA 709
          ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||| | |||||
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Db    615 CAACG------TCAGTGAGGCAGATGACAGTGTTCAATTCCAGCATATAATGGTGGGTCCATCCTA 659
          |||||      ||||||||||||| ||||| ||||||||||||||||||||||||||||||| ||

Qy    710 CCCCGATAGCCTGTGGATGTGTGGTGTT 769
          |||| ||||||||||||| ||||||||
Db    660 CCCCAATGACTTGTGGGTGGTGTTCCAGTTGTTCCAGCACATCATGGTTGGCCTTATCCT 719

Qy    770 GCCCGGCATCGTCATCCTCTCCTGTTACTGCATCATCTCTAAGCTGTCACACTCCAA 829
          || ||| ||||| |||||||||||||||| || | |||||||||| ||||||||||
Db    720 GCCTGTATTGTCATCCTGCTATTGCATTATCATCCCAAGCTGTCACACTCCAA 779

Qy    830 GGGCCACCAGAAGCGCAAGGCCCTCAAGACGCCCTCCAGCGTCATCCTAGCTTCTTTGC 889
          |||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||||
Db    780 GGGCCACCAGAAGCGCAAGGCCCTCAAGACCATCCTCATCCTGCTTTCTTCGC 839

Qy    890 CTGCTGGCTGCCATTATGGGGATCAGCATCCTTCATCCTTTGGGAGTCAT 949
          || |||| |||||||||||||||||| |||||||||||| |||||||||||
Db    840 CTGTTGGCTGCCTTACTACATTCAGCAGCATCAGCATCCTTCATCCTCTGGAAATCAT 899

Qy    950 CAAGCAAGGATGTGACTTCGAGAGCATTGTGCACAAGTGATCTTCCATCACAGAGGCCCT 1009
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    900 CAAGCAAGGGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCCATCACCGAGGCCCT 959

Qy   1010 CGCCTTCTTCCACTGTTGCCTCGAACCCCATCCTCTATGCCTTCCTCGGGGCCCAAGTTCAA 1069
          |||||||||||||||||||||||||| ||||||||||||||| ||||| |||||||||||
Db    960 AGCTTTCTTCCACTGTTGTCTGAACCCCATCCTCTATGCTTTCCTGGGAGCCCAAATTTAA 1019

Qy   1070 AAGCTCTGCCCAGCATGCACTCAACTCACTCATGAGCAGAGGCTCCAGCCTCCAGAATCCTTTC 1129
          |||||||||||||||||| ||||||| ||||||||||||||||||||||| ||||||||||
Db   1020 AACCTCTGCCCAGCACGCCACCTCTTTCCGTTCCACCTGTCTGAGCAGGGTCCAGCCTCCAGAGATCCTCTC 1079

Qy   1130 CAAAGGAAGCGGGTGACACTCTTCCGGTCTCCACGGAGTCAGAATCCTCCAGTTTCA 1189
          |||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 CAAAGGAAAGCGAGTGGACATTCAGTGGGACACCGCCACCGAGTCTTCAAGTTTTCA 1139

Qy   1190 CTCCAGTCAACCCCTATGCAAAGACTTATATAATATATATATATATAAAGAACTT 1249
          ||||||                || |||||  || ||  ||||||||||||||||
Db   1140 CTCCAGCTAA-------CACAGATGTAAAAGACTTTTTTTTTACGATAAATAACTTTT 1191

Qy   1250 TTTTATGTTACACATTTCCAGATATAAGACTGACCAGTCTCTGTACAGTTTTTTTTT 1309
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db   1192 TTTAAGTTACACATTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTTTATTGC 1251

Qy   1310 TTTTTAATTGACTGTTGGGGAGTTTATGTTCCTCTAGTTTTTGTGAGGTTTGACTTAATTT 1369
          |||||||||||||||||||||||                ||||| |||||||||||||||
Db   1252 TTGTTGGATTTTTGT------CTTCGTGTTTCTTTAGTTTTTGTGAAGTTTAATTGACTTA 1305

Qy   1370 ATATPAAATATTGTTTTTTGTTGTTCATGTGAATGAGGCGTCTAGGCAGGACCCTGTGGCC 1429
          |||||||||||| ||||| || ||| | || |||| || |||||||||||| |||||||||
Db   1306 TTTATA---TAAATTTTTTGTTTCATATTGATTGTGTCTCTAGGCAGGACCTGTGGGCC 1361

Qy   1430 AAGTTCTTAGTAGCTGTTTATCGTGTGTAGGACTGTAGAACTGATGAGAAAACTGA 1489
          |||||||||||| ||||||||||||||||||||||||||||      |||||||||
Db   1362 AAGTTCTTAGTGTGCTGTATGTCTCGTGGTAGGACTGTAGAA------AAGGAACTGA 1413

Qy   1490 ACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTGCAGCTGTTGCTGCA 1549
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db   1414 ACATTCCAGACGCGTGTAGTGAATCACGTAAAGCTAGAAATGATCCCCGAGCTGTTTATGCA 1473

Qy   1550 TAAATCTTCATTCCGGAGGAGCACACCCCCACCCCCACCCCCCATTCTTAAAT 1609
          || ||||||||||||||||||||||  ||||||||||||||||||||| |||||
Db   1474 TAGATAATCTCTCCA------AAGGGAGCACACCCCCACCCCCACCCCCCATTCTTAAAT 1488

Qy   1610 TGTTTGGTTATGCTGTGTGATGGTTTGGTTTTTTTGTGTTGTGTTGTTTT 1669
          ||||||||||||||||||||| ||||||| ||| |||||||||||||||||
Db   1489 ------------TTCCCGTGGAACGTTTTTCCTGTTCTTAAGACGTGAT 1525

Qy   1670 TTTTCTGTAAAAGATGGCACTTAAAACCAAAGCCTGAAATGGTGTGGTAGAAATGCTGGGGT 1729
          |||  |||| ||||| ||||||||||| |||||| ||||||||||||  | ||||||||
Db   1526 TTTGCTGTGTAGAAGATGGCACTTATAACCAAAGCCCAAAGTGGT-ATAGAAATGCTGG--- 1581

Qy   1730 TTTTTTGTTTGTTTGTTTTTCAGTTTTCAAGTAGTGATTTGACTTCAGTTCCCTACAAAT 1789
          |||  ||||| ||| ||||||||||||||||||||| |||||||||||||||||||||| |
Db   1730 CGACGTCAGCCAGGGGACATCAGTCAGGCGGGGATGACAGGTACATCTGTGACCGGCCTTTA 709
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Db   1582  --------------------TTTTTCAGTTTTCAGGAGTGTGGTTGATTTCAGCACCTAC-AGT 1623

Qy   1790  GTACAGTCTTGTATTACATTGTTAATAAAAGTCAATGATAAACTTAAAAAAAAAAAAAA 1849
           |||||||||||||||||||||||||| |||  |||||||||||||  ||||||||||
Db   1624  GTACAGTCTTGTATTAAGTTGTTAATAAAAGTACATGTTAAACTTAAAAAAAAAAAAAA 1683

Qy   1850  AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1877
           |||||||||||||||||||||||||||||
Db   1684  AAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1711
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RESULT 4
US-10-723-860-5773
; Sequence 5773, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5773
; LENGTH: 1826
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-5773

Query Match   51.7%; Score 970; DB 8; Length 1826;
Best Local Similarity   76.1%; Pred. No. 3.5e-210;
Matches 1386; Conservative   0; Mismatches 300; Indels 136; Gaps   10;

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Qy    644  CTTTGCGACGTCAGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACATCGTGACCG 703
           ||||||||||||||||| ||||||||
Db    624  CTTTGCCAACG-------------TCAGTGAGGCAGATGACAGAGATATCGTGACCG 668
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Qy     44  GCAGGTGCAGGTAGCAGTGACCCTCGAGGCGTTTGGTGCTCCGTAACCACCACGGCTG 103
           |||| |||||||| ||| ||||  ||||||  | |||  ||||||||| ||||
Db     29  GCGGGCAGGCAGGTAGCAAAGTGACCGCGAGGGCCTGAGTGCTCCAGTAGCCACCGCATCTG 88
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Qy    422  CAGTCCATGTCATCTACACAGTCAACCTCTCAGCAGTGTCCTCATCCTCTGCCTTCATCA  481
           ||||||||||||||||||||||||||||||||||||||  |||||||| ||||||||||||
Db    517  GCCTGGACGGTACCTGCCATTGTCCACGCCACCAACAGTCAAAGGCCAAGGAAACTGC    576

Qy    482  GTCTTGGACCGCTACCTGGCCATCGTCCAGCGCCACCAACAGTCAAAGTGT-ATAGAAATGC  541
           ||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    577  TGGCTGAAAAGGCAGTCATGTGGGCGTCATGTGGGCGTCCTGACTATACCTG    636

Qy    577  TGGCTGAAAAGGTGTCATGTGGCGTCTGTGATCCGCCCTCCTCGTGACTATTCCGG  636
           ||||||||||||||||||||||||||||||||
Db    637  ACTTCATCTTTGCCACGTCAGCGTCAGTCAGGGGGATGACAGGTACATCT    696

Qy    637  ACTTCATCTTTGCCACGTCAGGGGGATGACAGGTACATCT-------TCAGTGAGGCAGATGACAGATATATCT  696
           ||||||||||||||
Db    697  GTGACCGCCTTACCCCGATAGCCTGTGGATGGTGGTGTTTCAATTCCAGCATATAATGG    756

Qy    697  GTGACCGCCTTACCCGATAGCTGTGGATGGTGGTGTTTCAATTCCAGCATATAATGG  756
           |||||||||||||||||||||||||||||||||||||||
Db    757  GTGACCGCTTCTACCCCAATGACTTGTGGTGGTTTGTGTTCAGCACATCATGG    706

Qy    757  TGGGTCTCATCCTGCCGGCATCGTCATCCTCCCTGTTACTGCATCATCATCCTAAGC  816
           |||||||||||||||||||||||||||||||||
Db    707  TTGGCCTTATCCTGCCTGTATTGTCATCCTCGTGCTGTTATTGCATCATCCTCCAAGC    766

Qy    817  TGTCACACTCCAAGGCCACCAGAGACGCAAGGCCCTCAAGACAGACAGTCATCCTCATCC  876
           ||||||||||||||||||||||||||||||||||||
Db    767  TGTCACACTCCAAGGGCCACCAGAGACGCAAGGCCCTCAAGACCAGACCACAGTCATCCTCATCC    826

Qy    877  TAGCTTCTTTGCCTGCTGCGCCGCATATATGTGGGATCAGATCAGCATCGGACTCCTCATCC  936
           |||||||||||||||||||||||||||||
Db    827  TGGCTTTTCTTCGCCTGTTGCTGCCTTACTACATTGGGATCAGCATCAGGACTCCTCATCC    886

Qy    937  TTTTGGGAGTGCATCAAGCAGATGTGACTTCGAGACGTTCTGAGAGCATTGTGCACAAGTGGATCTCCA  996
           || ||||||||||||||||||||||||||
Db    887  TCCTGGAAATCATCAAGCAAGGGTGTGAGTTGAGAACACTGTGCACAAGTGGGATTTCCA    946

Qy    997  TCACAGAGGCCCTCGCCTTCTTCCACTGTTGCCTGGCCATCTCACTCCCCATGTCCTTCCTCG  1056
           |||||||||||||||||||||||||||||||||
Db   1007  GAGCCAAATTTAAAACCTCTGCCCACGCACCTCACCTCTGTGAGCAGAGGGTCCAGCC    1066

Qy   1057  GGGCCAAGTCAAAAGCTCTGCCGCCAGCATGCACTCCAACTCCAACTCAACTCAGAGCGCTCAAGCC  1116
           |||||||||||||||||||||||||||||||||||||
Db   1007  GAGCCAAATTTAAAACCTCTGCCCAGCACGCACCTCACCTCTGTGAGCAGAGGGTCCAGCC    1066

Qy   1117  TCAAGATCCTTTCACTCCAAAGGAAAGCCGGGGGTGGACACTCTTCCGTCTCCACGGAGTCGGAAT  1176
           ||||||||||||||||||||||||||||||||||
Db   1067  TCAAGATCCTCCAAAGGAAAGCCAGCGAGGTGGACATTCATCGTGTTTCCACTGTCTCGAGT    1126

Qy   1177  CCTCCAGTTTCACTCCAGCTAACCCTTATGCAAAGACTTATATATATATATATATATA  1236
           |||||||||||||||||
Db   1127  CTTCAAGTTTTCACTCCAGCTAA------CACAGTGTAAAAGACTTTTTTTTATACG    1178

Qy   1237  TGATAAAGACTTTTTTATGTTACACATTTTCCAGATATATAGGAGACTGACCAGTCTTGTA  1296
           ||| ||||||||||||||||||||||
Db   1179  ATAAATAACTTTTTTTTAAGTTACACATTTTTCAGATATAAAAGACTGACCAAATATTGTA    1238

Qy   1297  CAGTTTTTTTTTTTTTTTTGTTTAATTGACTGTTGTGGGAGTTTAATTGTTCCTCTAGTTTTTGTGAGG  1356
           |||| ||||||||||||
Db   1239  CAGTTTTTATTGCTTTGTTGTGATTTTTGT-----CTTGTGTTTCTTTAGTTTTTTGTGAAG    1292

Qy   1357  TTTGACTTAATTTATATAAAATATTGTTTTTTGTTTTCATGTGAATGAGCGTCTAGGC  1416
           ||||||||||||||  ||
Db   1293  TTTAATTGACTTATTTATA---TAAATTTTTTTTTTTGTTTCATATTGATGTGTGTCTAGGC    1348

Qy   1417  AGGACCTGTGGCCAAGTTCTTAGTAGCTGTTATCGTGTGTAGGACTGTGTAG  1476
           ||||||||||||||||||||||||||||||||||||||||
Db   1349  AGGACCTGTGGCCAAGTTCTTTAGTTGCTGTATGTCGTGTAGGACTGTAGAA-------    1402

Qy   1477  AGGAAGAAACTGAACATTCCAGAATTGAATGTCGTGTAAATTGAATAAAGCTAGCCGTGATCCTC  1536
           ||||||||||||||||||
Db   1403  --AGGGAACTGAACATTCCAGACGCGTAGTAGTCACGTAGTGAATCACGTAGAAATGATCCCC    1460

Qy   1537  AGTCTGTGCTGCATAATCCTTCATTCCGAGGAGCACCCCCCACCCCCAC  1596
           |||||||||||||||||||||
Db   1461  AGCTGTTTATGCATAGATAATCTCTCCA-----    1488
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Query Match        51.4%;  Score 964.2;  DB 8;  Length 1699;
Best Local Similarity  75.7%;  Pred. No. 7.1e-209;
Matches 1385;  Conservative 0;  Mismatches 308;  Indels 136;  Gaps 10;

Qy     37  CGCCCGGCGGCAGGTGCAGGTAGCAGTGACCCTCTGAGGCGTTTGGTGCTCCGGTAACCACC  96
           ||||||||||||||||||||||||||||
Db      7  CGTCCGCGGACGCGTGGGCGGACGCGTGGGGCCCGAGGCGCTCGAGGTCTCCAGTAGCCACC  66

Qy     97  ACGGCTGTAGAGCGGAGTGTTGCCATGGCAACCGATCAGTGTGAGTATATACACTTCTGTA  156
           ||||||||||||||||||
Db     67  GCATCTGGAGAACCAGCCGTTACCATGGA-----GGGGATCAGTATATACACTTCAGATA  121

Qy    157  ACTACTCTGAAGAAGTGGGGTCTGGAGACTATGATGCATGCAACAAGGAACCCTGCTTCCGGG  216
           ||||| ||||||||||||||||||||
Db    122  ACTACACCGAGGAAATGGGCTCAGGGGACTCAGGGACTATGACTCAGAAGAACCCTGTTTCCGTG  181

Qy    217  ATGAAAAGTCCATTTCAATAGAATCCATTTCAATAAAATCTTCTGCCCACCATCTACTTCATCATCTTCTGA  276
           |||||||||||||||||||||||||||||||||
Db    182  AAGAAAATGCTAATTTCAATAAAATCTTCTGCCCACCATCTACTTCCATCATCTTCTTAA  241

Qy    277  CTGGCATAGTGCGAATGGATTCGGCGAATGGATTGTGATCGGTCATGGGTTCAGGAGAAGCTAAGGA  336
           ||||||||||||||||||||||
Db    242  CTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAGAAGAAACTGGAAA  301

Qy    337  GCATGACGGACAAGTACCGGCTCACCTGCAGTGCTGACCTCCTCTTTGTCATCACAC  396
           |||||||||||||||||||
Db    302  GCATGACGGACAAGTACAGGCTCACCTGCACCTGCAGTTGCCACCTCTCCTCTTTTGTCATCATCACGC  361

Qy    397  TCCCCTTCTGGGCAGTTGATGCCATGGCCATGGCCATGGCTGACTGTGACTTTGGGAAATTTTTGTGTAAGG  456
           ||||||||||||||||||||
Db    362  TTCCCTTCTGGGCAGTTGATGCCGTGCGCAAACTGTGACTTTTGGGAACTTCCTATGTCAAGG  421

Qy    457  CTGTCCATATCATCTCACACTACACTCTCACAAGCCTCTACAGCAGCCGTTCTCATCCTCTGGCCTTCATCA  516
           ||||||||||||||||||
Db    457  ...
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Qy   1664  TTTTTTTTTTCTGTAAAGATGGACTTAAAACCAAAGCCTGAAATGGTGGTAGAAATGC  1723
           ||||||||||||| ||  |||||||||
Db   1535  CGTGATTTTGCTGTAGAAGATGGCACTTATAACCAAAGCCCAAGTGT-ATAGAAATGC  1593

Qy   1724  TGGGGTTTTTTTTTTGTTGTTTTTCAGTTTTCAGGAGTTGATTGACTTCAGTCCCT  1783
           ||||||||||||||
Db   1594  TGG-------TTTTTCAGTTTTCAGGAGTGGGTTGATTGACTTCAGCACCT  1633

Qy   1784  ACAAATGTACAGCTCTGTATTACATTGTGTAATAAAGAAAGTCAATGATAAAACTTAAAAAAAA  1843
           ||||||||||||
Db   1634  AC-AGTGTACAGCTCTTGATTAAGTTGTTAATAAAGTACATGTTTAAACTTAAACTTAAAAAAAAAA  1692

Qy   1844  AAAAAAAAAAAAAAAAA  1865
           |||||||||||||||||
Db   1693  AAAAAAAAAAAAAAAAA  1714
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Qy   1597 CCCATTCTTAAATTGTTTGGTTATGCTGTGTCGTGATGGTTGTTTGGTTTTTTTTTTGTGTT 1656
          ||                          ||      ||||||  ||||||||  ||
Db   1489 ------------------------------TTCCCGTGGAACGTTTTTCCTGTT 1512

Qy   1657 GTTGTTGTTTTTTTTTCTGTAAAGATGGCACTTAAACCAAAGCCTGAAATGGTGGTA 1716
          ||||  |||||||||||||||||||||||  ||||||||||||||||||||  ||  ||
Db   1513 CTTAAGACGTGATTTTGCTGTGTGAGAGATGGCACTTATAACCAAAGCCCAAAGTCGT-ATA 1571

Qy   1717 GAAATGCTGGGGTTTTTTTGTTTGTTTGTTTTTCAGTTTTCAGGAGTAGATTGACTTC 1776
          ||||||||||||                    |||||||||||||||||||||||||||
Db   1572 GAAATGCTGG-----------------------TTTTTTCAGTTTTCAGGAGTGGGTTGATTTTC 1611

Qy   1777 AGTCCCTACAAATGTACAGTCTGTATTACATTGTTAATAAAAGTCAATGATAAACTTAA 1836
          |||||||||||||||||||||||||||||||||||||||||  |||||||||
Db   1612 AGCACCTAC-AGTGTACAGTCTTGTATTAAGTTGTTAATAAAAGTACATGTTAAACTTAA 1670

Qy   1837 AAAAAAAAAAAAAAAAAAAAAAAAAA 1865
          ||||||||||||||||||||||||||
Db   1671 AAAAAAAAAAAAAAAAAAAAAAAAAA 1699


RESULT 6
US-10-706-265-11
; Sequence 11, Application US/10706265
; Publication No. US20040132642A1
; GENERAL INFORMATION:
; APPLICANT: Hwang, Sam
; TITLE OF INVENTION: METHODS OF INHIBITING METASTASIS OR GROWTH OF A TUMOR CELL
; FILE REFERENCE: 224738
; CURRENT APPLICATION NUMBER: US/10/706,265
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 60/425,472
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/511,581
; PRIOR FILING DATE: 2003-10-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-706-265-11

  Query Match      51.2%;  Score 960.4;  DB 7;  Length 1662;
  Best Local Similarity  76.3%;  Pred. No. 5.1e-208;
  Matches 1371;  Conservative   0;  Mismatches  291;  Indels 136;  Gaps  10;

Qy     68 CTGAGGCGGTTGGTGCTCCGGTAACCACCACGGCTGTAGAGGCAGAGTGTTGCCATGGAACC 127
             |  |||  ||||||||||||  ||||  |||||||||  ||||||  |||||||||
Db      1 CCGAGGGGCCTGAGTTCCACTGAGTCTTCCAGTAGCCATCTGGAGAACCAGCCAGCGGTTACCATGGA-- 58

Qy    128 GATCAGTGTGAGTAATATATACTTCGATAAAGTACTTCTGAAGAAGGGGGTCTGGAGACTA 187
          ||||||  ||  ||||| |||||||||||| || |||||||||  |||| | ||| ||  ||
Db     59 --GGGGATCAGTAGTATACACTTCAGATAACTACACCGAGAATCAGCCGAAATGGGCTCAGGGGACTA 115

Qy    188 TGACTCCAACAAGGAACCCGCTTCCGGGATGAAAACGTCCATTTCAATTTCAATAGGATCTTCCT 247
          ||||||||||||||||||||||||  |||||||||  | || |||||  |||||  |||||
Db    116 TGACTTCCATGAAGGAACCCGTTTCCGTGAAGAAAAATGCTAATTTCAATAAAATCTTCCT 175

Qy    248 GCCCACCATCACTTCATCATCTTCTTGACTGGCATAGTCGGCAATGCAATGGTTGGTGATCCT 307
          ||||||||||||||||||||||||  |||||||||||||  ||||| |||| |||||||||
Db    176 GCCCACCATCACTTCCATCATCTTCTTAACTGGCATTGGTTGGGCATTGTGTGGCAATGTGGTTCATCCT 235

Qy    308 GGTCATGGGGTTACCAGAAGAAGCTAAGGAGCATGACGGACAAGTACCGGCTGACCTGTC 367
          |||||||||||||||||||||||||||| ||||| || ||||| || |||||||||||||
Db    236 GGTCATGGGGTTACCAGAAGAAGCTGAGAGCATGACGGACAAGTACCGGCTGACCTGTC 295

Qy    368 AGTGGCTGACCTCCTTTTGTCATCACACCCCCCTTCTGGGGCAGTTGATGCCATGGCTGA 427
          |||||||||||||||||| ||| |||||||||||||| |||||||||||||| |||
Db    296 AGTGGCCGACACTTCCTCTTTGTCATCACGCGTTGTCATCACACGTGCAGTTGGTCCGTGGCAA 355

Qy    428 CTGGTACTTTGGGAAAATTTGTGTAAGGCTGTCCTATATCATCTTACACACGTCCAACCTCTA 487
          |||||||    |||||||      ||||||||  ||  ||        |||||   ||
Db   1508 TAAATTGAATAAAGCTGGTGCTGTCGTGATCACTCGTGCTGTCATTCCGAG 1567
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Db    356 CTGGTACTTTGGGGAACTTCCATCTGCCTTCCTATGCAAGCAGTCCATGTCATCACAGTCAACCTCTA 415
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    415

Db    488 CAGCAGCGTTCTCATCCTCGGCCCTCATCAGCTGACCGGTACCTCGCCATTGTCCACGC 547
          ||||||||| |||||||||||||||||||||||||||||||||| ||||||||||||
Qy    416 CAGCAGTGTCCTCATCCTCGGCCTTCATCAGTCTGGACCGCTACCTGGCATCGTCCACGC 475

Db    548 CACCAACAGTCAAAGGCCAAGAGAAACTGCTGGCGGAGAAGCAGTCTATGTGGGCGCTG 607
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    476 CACCAACAGTCAGAGGCCAAGGAGAGGCTGGTGCTGAAAAAGGTGGTCTATGTGGGCGCTG 535

Db    608 GATCCCAGCCCTCCTGCGACTATACCGACTATCTTGCGACGTCAGCCAGGGGGA 667
          |||||||||||||||||||||||||||||||||||||||| |||
Qy    536 GATCCCTGCCCTCCTGCGACTATACCGACTATCTTCATCTTTGCCAACG 582

Db    668 CATCAGTCAGGGGATGACAGGTACATCTGGACGGTACATCTGTGACCGGCCTTACCCCCGATAGCCTGTGGAT 727
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    583 --TCAGTGAGGCAGATGACAGATATATCTGTGACCGGCCTTCTCACCCAATGACTGTGTGGGT 640

Db    728 GGTGTGTGTTCAATTCCAGTTTCAGCACATCATCATCTCTAAGTCCAACCTCCAAGGCACACTCCAAGAGGCGCAA 787
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    641 GGTTGTGTGTTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGTGCCTTGGTGTATTGTCATCCT 700

Db    788 CTCCTGTTACTGACATCATCATCTCTTAGTCCAACCTCCAAGGCCACACTCCAAGAGGCGCAA 847
          ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Qy    788

Db    848 GGCCCTCAAGACGACAGTCATCCTCCTAGCTTCTCTTGCCTGTCGCTGGCTGCCTACTATATTA 907
          |||||||||||||||||||||||||||||||||||| || |||||||| ||||||
Qy    701 GTCCTGCTATTGCATTTATCATCTCCAAGCGTCAACAGTCAACACTCCAAGGGCACCAAGCGCAA 760

Db    908 TGTGGGGATCAGCATCGACTCCTTTTTGGGAGTGCCATCAAGCCAGTCATGTGACTT 967
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    848 GGCCCTCAAGACCACCAGTCATCCTCCTAGCTTTCTTTGCCTCTTGGCTGCCTTACTA 907

Db    968 CGAGAGCATGTGCACAAGTGGATCCTTCCATCACAGAGCCCCTCGCCTTCTTCGCCCACTGTTG 1027
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    908 TGTGGGGATCAGCATCAAGCAGCTCATCAAGCAAGCAAGAATCATCAAGCAAGCAAGGGTGTGAGTT 967

Db   1028 CCTGAACCCCATCCTCTATGCCTTCCTCGGGGCCAAGTTCAAAAGCTCTGCCCCAGCATGC 1087
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    968 CGAGAGCATGTGCACAAGTGGATCCTTCCATCACAGAGCCCCTCGCCTTCTTCGCCCACTGTTG 1027

Db   1088 ACTCAACTCCATGAGCAGCAGCCTCAGAATCCTTTCCAAGATCCTTTCCAAAGGAAGGAAGGCGGGGTGG 1147
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1028 TGAGAACACTGTGCACAAGTGGATTTCCATCACCGAGCCCCTCAGCTTTTCTTCCCACTGTG 940

Db   1001 ACTCACCTCTGTGAGCAGAGGGTCCAGCCTCCAGATCCTCTCCAGTTTCACTCAGCTAA------ 1060
          |||||||||||||||||||||||||||||||||||||||||| || |||||||||
Qy   1088 ACTCAACTCCATGAGCAGCAGCCTCAGAATCCTTTCCAAGATCCTTTCCAAAGGAAGGAAGGCGGGGTGG 1147

Db   1148 ACACTCTTCCGTCTCCACGAGTCAGAATCCTCCCAGTTTTCACTCCGCTAA----- 1207
          |||| || || ||||| |||| |||| ||| ||||| || |||||||| ||
Qy   1061 ACATTCATCTGTTTCCACTGAGTCTTCAAGTTTCAAGTTTCACTCAGCTAA------ 1112

Db   1208 CAAAGACTTATATAATATATATAATATATGAAAGAACTTTTTTTATGTTACACATTTT 1267
          ||||||||| |||||||||||||| || |||| |||| || |||| |||||| ||||
Qy   1113 CACAGATGTAAAAGACTTTTTTATTTTATACGATAAATAACTTTTTTTTTAAGTTACACATTTT 1172

Db   1268 CCGAGATATAAGACTGACCAGTCTTGTACAGTTTTTTTTTTTTTGTTGGTTGACTGTTGG 1327
          ||||||||||||||||||||||||||||||||||||||||||||  |||||| ||
Qy   1173 TCAGATATAAAAGACTGACCAAATATTGTACAGTTTTTATTGCTTTGTGGATTTTGT---- 1229

Db   1328 GAGTTTTATGTTCCTCTAGTTTTTGTGAGGTTTGACTTAATTTATATAAATATTGTTTTTT 1387
          ||||||| ||||||||||||||||||||  |||| |||| ||  ||||||||||
Qy   1230 ---CTTGTGTTTCTTTAGTTTTGTGAAGTTTAATTGACTTATTTTATA----TAAATTTT 1282

Db   1388 GTTTGTTTCATGTGAATGAGCGGTCAGGGCAGGAGCAGTCTCAGTTTCTTCAGTAGCTGTT 1447
          ||||||||||||||||||||||| || |||| ||||| ||||||||| ||||||||||||
Qy   1283 TTTTGTTTCATATTGATGTGTCTCAGGCAGGAGCCAAGTTTCTTAGTTGTTGCTGTA 1342

Db   1448 TATCTGTGTGGACTGTAGAACTGTAGAGGAGGAAGAAACTGAACATTCCAGAATGTGTGG 1507
          |||||||||||||||||||||| ||||||||||||||||||| || ||||
Qy   1343 TGTCTCGTGGTGGACTGTGAGAA----------AAGGGAACTGAACATTCCAGAGCGTGTAG 1394

Db   1508 TAAATTGAATAAAGCTGGTGCTGTCGTGATCACTCGTGCTGTCATTCCGAG 1567
          ||||||             ||    |||      |   ||||
Qy   1428 CTGGTACTTTGGGAAAATTTGTGTAAGGCTGTCCTATATCATCTTACACACGTCCAACCTCTA 487
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Db   1395  TGAATCACGTAAAGCTAGAAATGATCCCAGCTGTTTATGCATAGATAATCTCTCCA--  1451
                  ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Qy    307  GGACAAGTACAGGCTGCACCTGTCAGTGGCTGGACACCTCCTCTTTGTCATCACGCTTCCCTT  366

Db   1568  GAGCACCCCACCCCACCCCCCACCCCCCATTCTTAAATTGTTTCGGTTATGCTGTGT  1627
                  |||||||||||
Qy    404  CTGGGCAGTTGATGCCATGGCTGGTACTTGGGAAATTTTGTGTAAGGCGTGTCCA  463

Db   1452  -------                                                  1451
                  ||||||||
Qy    367  CTGGGCAGTTGATGCCGTGGCTGCAAACTGGTACTTGGGAACTTCCTATGCAAGGCAGTCCA  426

Qy   1628  GATGGTTTGTTTGGTTTTTTTGTGTTTGTTGTTTTTCTGTAAAAGATGC  1687
                  ||||    |||   ||||||||||||||||
Db   1452  ------TTCCCGTTGGAAACGTTTTCCTGTTCTTAAGACGTGATTTTGCTGTAGAAGATGC  1506
                  TGTCATCTACAGTCAACCTCTACAGCAGTCGTTCATCGTCCTCGGCCTTCATCAGTCTGGA  486

Qy   1688  ACTTAAAACCAAAGCCTGAAATGGTGGTAGAAATGCTGGGGTTTTTTTGTTTTGTTTGTT  1747
                  |||||||||||   |||||||||||
Db   1507  ACTTATACCAAAGCCCAAAGTGT-ATAGAAATGCTGG-------------T  1545
                  |||||||||||||   |||||||||||||   ||||||||||||
Qy   1748  TTTTCAGTTTTCAAGAGTAGAATTGACTTCAGTCCCTACAAATGCACAGTCTTGTATTACA  1807
                  ||||||||||| ||||     ||| |||||||||||||||||||||||||||
Db   1546  TTTTCAGTTTTCAGGAGTGGGTTGATTTCAGCACCTAC-AGTGTACAGTCTTGTATTAAG  1604

Qy   1808  TTGTTAATAAAAGTCAATGATAAACTTAAAAAAAAAAAAAAAAAAAAAAAAAA  1865
                  ||||||||   ||||||     |||||||||||||||||||||||||||||||
Db   1605  TTGTTAATAAAAGTACATGTTAAAACTTAAAACTTAAAAAAAAAAAAAAAAAAAAAAAAAA  1662
```

RESULT 7

US-10-151-274-14

; Sequence 14, Application US/10151274

; Publication No. US20030064071A1

; GENERAL INFORMATION:

; APPLICANT: Littman, Dan R.

; APPLICANT: Kwon, Douglas S.

; APPLICANT: van Kooyk, Yvette

; APPLICANT: Geijtenbeck, Tneo

; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY

; TITLE OF INVENTION: INTO

; TITLE OF INVENTION: CELLS

; FILE REFERENCE: 1049-1-017

; CURRENT APPLICATION NUMBER: US/10/151,274

; CURRENT FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: US/09/517,605

; PRIOR FILING DATE: 2000-03-02

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.0

;

; SEQ ID NO 14

; LENGTH: 1679

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-151-274-14

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Query Match     50.8%;  Score 952.8;  DB 5;  Length 1679;
Best Local Similarity  80.2%;  Pred. No. 2.8e-206;
Matches 1210;  Conservative  0;  Mismatches 252;  Indels 46;  Gaps  6;
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Qy    44  GCAGGTGCAGGTAGCAGTGACCCTCTGAGGCGTTTGGTGTCTCCGGTAACCACCACGGCTG  103
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    12  GCGGCAGCAGGTAGCAAAGTGACGCCGAGGCCCTGAGGTGCTCCAGTAGCGCACCGCATCTG  71

Qy   104  TAGAGCGAGTGTGCCATGGAACCGATCAGTGTGAACCAGTGTGAGTATATACACTTCTGATAACTACTC  163
                  |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    72  GAGAACCAGCGCGTTACCATGGA-----GGGGATCAGTAATCAGTATATACACTTCAGATAATAACTACAC  126

Qy   164  TGAAGAGTGGGGTCTGGAGACTATGACTTCCAACAAGGAACCCTGCTTCCGGGATGAAAA  223
                  ||||||| ||| |||||||||||||||||||||||||||||
Db   127  CGGAGGAAATGGGCTCAGGGGCTCAGGGGGACTATGACTTCCATGGAAGGAACCCTGTTTCCGTGAAGAAA  186

Qy   224  CGTCCATTTCAATAGGATCTTCCTGCCCACCAATCTACTTCATCATCTTCTTGACTGGCAT  283
                  |||  ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   187  TGCTAATTTCAATAAAATCTTCCTGCCCACCAATCTACTCATCATCTTCTTAACTGGCAT  246

Qy   284  AGTCGGCAATGCATGGTGTCATCCTGGTTCATCGGGTTACCAGAAGAAGCATGAC  343
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   247  TGTGGGCAATGGATTGGTCATCCTGGTCATGGGGTTACCAGAGAAGAAACTGAGAAGCATGAC  306

Qy   344  GGACAAGTACCGGCTGCACCTGTCAGTGGCTGCGAACCTCCTCTTTGTCATCACACTCCCCTT  403
                  | |
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Db   1354 GTGGCCAAGTTCTTAGTTGCTGTATGTCTCGTGTGTAGAA-------AAGGG 1405
Qy   1484 AACTGAACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTT 1543
          ||||||||||||||||| |||| |||| ||||||||| ||||||||| |||||| |||||
Db   1406 AACTGAACATTCCAGAGCGTGTAGTGTGAATCACGTAAAGCTAGAAATGATCCCCAGCTGTT 1465

Qy   1544 GCTGCATA 1551
          ||||||||
Db   1466 TATGCATA 1473
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RESULT 8
US-10-225-567A-75

; Sequence 75, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRNT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-75

Query Match   50.8%;   Score 952.8; DB 5; Length 1679;
Best Local Similarity 80.2%; Pred. No. 2.8e-206;
Matches 1210; Conservative 0; Mismatches 252; Indels 46; Gaps 6;

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Qy     44 GCAGGTGCAGTGAGCAGTGACCCTCTGAGCGCGTTGGTGCTCCCGTAACCACCACGGCTG 103
          ||  || ||||||||| | |||| | |||| |||| ||| |||| ||| ||| |||||||
Db     12 GCGGCGCAGGTAGCAAAGTGACCGCGAGGGCCTGAGTCGCTCCAGTAGCCACCGCCATCTG 71

Qy    104 TAGAGGCGAGTGTTGCCATGGAACCGATCAGTGTGAGTATATACACATTCTGATAACTACTC 163
          |||||||||||||| ||||| |||||||||||||| ||||||||||||     ||||||||
Db     72 GAGAACCAGCGGTTACCATGGA-----GGGGATCAGTATATACACATTCAGATAACTACAC 126

Qy    164 TGAAGAAGTGGGGTCTGGAGACTATGACTCCCAACAAGAACCTGCTTCCGGATGAAAA 223
          |||||||||||| |||||||||||||||||| || ||| || |||||||||||||| |
Db    127 CGAGGAAATGGGCTCAGGGACTATGACTCCATGCAAGAACCCGTTTCCGTGAAGAAAA 186

Qy    224 CGTCCATTCAATAGGATCTTCCTGCCCACCATCACTTCATCATCTTCTTGACTGGCAT 283
          ||| |||||||| || ||| ||||| |||||||| |||||||||||||||| ||||||
Db    187 TGCTAATTTCAATAAAATCTTCCTGCCCACCATCATCTTCTTCTTAACTGGCAT 246

Qy    284 AGTCCGGCAATGGATTGGTGATCCTGGTCATGGGTTACCAGGAAGCTGAAGGAGCATGAC 343
          |||| |||||||| ||||| |||||||||||||| |||||||||||||| |||||||||||
Db    247 TGTCAATTTCAATAAATCTTCCTGCCCACCATCATCTTCTTCTTAACTGGCAT 306

Qy    344 GGACAAGTACCGGCTGCACCTGCTGCAGTGCTCAGTGCTGACACTCCCCTT 403
          |||||||||||||||||||| || |||||| ||||| |||| |||||||||
Db    307 GGACAAGTACAGGCTGCACCTGTCAGTGCCGACCTGTCAGTGCCTTCCCTT 366

Qy    404 CTGGGCAGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTGTGTAAGGCGTGTCCA 463
          ||||||| || |||||||| || || |||||| |||||||| |||  ||||||||| || |
Db    367 CTGGGCAGTTGATGCCGTGTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCA 426

Qy    464 TATCATCTACACTGTCAACCTCACAGCAGCGCTTCCATCCTGGCCTTCATCAGCCTGA 523
          ||| || |||||| ||| |||| || || |||||||||| |||  |||||||||||||
Db    427 TGTCATCTACACAGTCAACCTCTACAGAGTGCTCCTCATCCTCGCCCTTCATCATCTCTGA 486

Qy    524 CCGGTACCTGCCCCATTGTCACGCCACCAACAGTCAAAGGCCAAGGAAACTGGCTGA 583
          |||| |||||| ||||||||| |||| |||| ||| |||||||||||| ||||||||
Db    487 CCGCTACCTGGCCATCGTCCACGCCACCAACAGTCAGAGGCCAAGGAAGAGAAGCTGTGTTGGCTGA 546
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Qy    584 AAAGGCAGTCTATGTGGGGCGTCTGACATCCTCCTGCTGCCGACTATCCTGACTTCAT 643
          ||||||||||||||||||||| |||||||||||| ||||||| |||||||||| ||||
Db    547 AAAGGTGGTCTATGTGGGGCGTCTGGATCCCGCCCTGCTGCCGACTATTCCGACTTCAT 606

Qy    644 CTTTGCGACGTCAGCAGCAGGGGACATCAGTCAGGGGGATGACAGTGACACGTACACCG 703
          |||||||||  |||||||||||| | |||||           |||||||||||||||||
Db    607 CTTTGCCAACG-----------TCAGTGAGGCAGCAGATGACACAGATAATCTGTGACCG 651

Qy    704 CCTTTACCCGATAGCCTGTGGATGGTGTGTTCAATTCCAGCATATAATGGTGGGTCT 763
          ||||||| || || || || |||||||| ||| |||||  ||||||| | || ||||
Db    652 CTTCTACCCCAATGACTTGTGGTGTTGTTCCAGTTTCAGTTTCATCATCTGGCTT 711

Qy    764 CATCCTGCCGGCATCGTCATCCTCCTGCTACTGCATCATCATCTCTAAGCTGTCACA 823
          |||||||| |||||||||||||||||| | ||||||||||||||||||| ||||||||
Db    712 TATCCTGCTGGTATTGTCATCCTGTCCTGCTATTGCATTATCATCTCCAAGCTGTCACA 771

Qy    824 CTCCAAGGGCACCAGAAGGCCAAGGCCCTCAAGACAGTACACAGCACCTCTCCTAGCTTT 883
          ||||||||||||||| |||||||||||||| ||| |||||||| ||| ||||||||||||
Db    772 CTCCAAGGGCACCAGAAGAAGGCCAAGGCCCTCAAGACCAGTACACAGTCATCCTCCTGGCTTT 831

Qy    884 CTTTGCCTGCTGGCTGCCATATTATGTGGGGGATCAGCATCGACTCCTCCTTCCTTTGGG 943
          ||||||||  |||||||| ||| || ||||| || ||||||||||||||| |||||| ||
Db    832 CTTCGCCTGTTGGCTGCCCTTACTACATTGGGGATCAGCATCGACTCCTCCTTCATCCTCCTGA 891

Qy    944 AGTCATCAAGCAAGGATGTGACTTCGAGACGTCATTGTGCACAAGTGATCATCCATCACAGA 1003
          ||||||||||||| || ||||| ||||| || |||||||||||||| ||  |||| |||||
Db    892 AATCATCAAGCAAGGTGTGAGTTTGAGACACTGCACAAGTGGATTTCCATCACCGA 951

Qy   1004 GGCCCTCGCCTTCTCCACTGTTGGCCTGAACCCACCCATCCTCATGCGCTTCCTCGGGGCCAA 1063
          |||||| |||||||||||| ||||||| || |||||||||||||| ||||| |||||||||||
Db    952 GGCCCTAGCTTCTTCCACTGTTGCCCACTGGAACCCCATCCTCATGCGTTGCTTCCTTGGAGCCAA 1011

Qy   1064 GTTCAAAAGCTCTGCCCAGCATGCACTCAACTCACTCCATGAGCAGAGGCTCCAAGCCTCAAGAT 1123
          |||||||  |||  |||| ||| |||| |||| |||||||||||||| || ||| | ||||||||
Db   1012 ATTTAAAACCTCGCGCCAGCAGCATGCACTCACCTGGTCGGAGCAGAGGGTCCGGCCTCCAAGAT 1071

Qy   1124 CCTTTCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGAATCCTCCAG 1183
          |||| |||| ||||||||| | |||||||||||| |||||||||||||| || |||||||
Db   1072 CCTCTCCAAAGGAAGCGGGTGGACATTCATCTGTTTCCACTGCTGGTCTTGAAG 1131

Qy   1184 TTTTCACTCCAGCTAACCCTTATGCAGAAGACTTATATAATATATATATGATAAA 1243
          |||||||||||||| ||  | |||| | | | |||||  |||| ||||| |||||
Db   1132 TTTTCACTCCAGCTAACAGATGTAACATACTTCAGATAACTACACAC-----TTTTATACGATAAATA 1183

Qy   1244 GAACTTTTTATGTTACACATTTCCAGATATAAGACTGACCAGTCTTGTACAGTTTT 1303
          ||||| |||| ||||||||||  ||||| ||  |||| ||||| | ||||||||||
Db   1184 ACTTTTTTTTAAGTTACACATTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTTT 1243

Qy   1304 TTTTTTTTTTAATTGACTGTGGGAGTTTATGTTTCCTCTAGTTTTTGTGAGGTTTGACT 1363
          |||||||||| |  || |||||     ||||||||||||| ||||||||||||||||| |
Db   1244 TATTGCTTGTTGGATTTTTGT------CTTGTGTTTTTTCTTTCATTTTGTTTCATATGTGTGAAGTTTAATT 1297

Qy   1364 TAATTTATATAAAATATGTTTTGTTGTTTCATGTGATGAATGAGGGTCTAGGCAGGACCTT 1423
          |||| || | |  |||  ||||||||||||||||| ||| |||||||||||||||||||||
Db   1298 GACTTTATTTATA----TAAATTTTTTTTGTTGTTTCATTTGTGTATGTGTCTAGGCAGGACCT 1353

Qy   1424 GTGGCCAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTAGAAACTGTAGAGGAAGA 1483
          |||||||||||||||||||||||  ||||||||||||| ||||| ||| |||||||||||||
Db   1354 GTGGCCAAGTTCTTAGTTGCTGTATGTCTCGTGTGTAGAA-------AAGGG 1405

Qy   1484 AACTGAACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTTCCA 1543
          |||||||||||||||| |  ||| | |||| ||||||||| ||||||||| |||||||||||
Db   1406 AACTGAACATTCCAGAGCGTGTAGTGTGAATCACGTAAAGCTAGAAATGATCCCCAGCTGTT 1465

Qy   1544 GCTGCATA 1551
          ||||||||
Db   1466 TATGCATA 1473
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RESULT 9
US-10-021-660-58
; Sequence 58, Application US/10021660

; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynne, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: EOS Biotechnology, Inc.
; TITLE OF INVENTION No. US20030152926A1el Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; TITLE OF INVENTION: Modulators
; FILE REFERENCE: 018501-00710US
; CURRENT APPLICATION NUMBER: US/10/021,660
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US/09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/637,977
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-021-660-58

Query Match   50.8%;   Score 952.8; DB 6; Length 1679;
Best Local Similarity   80.2%;   Pred. No. 2.8e-206;
Matches 1210; Conservative   0; Mismatches 252; Indels 46; Gaps 6;

```
Qy    44 GCAGGTGCAGGTAGCAGTGACCCTCTGAGGCGTTTGGTGCTCCGGTAACCACCACAGGCTG 103
            |||| ||||||||||||||||||||||  |||||| ||||||||||| |||||||||
Db    12 GCGGCAGCAGGTAGCAAAGTGACGCGAGGCCCTGAGGTGCTCCGGAGGCCTCCCAGTCATCTG 71

Qy   104 TAGAGCGAGTGGTGTTGCCATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTC 163
            ||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    72 GAGAACCAGGCGGTTACCATGGA-----GGGGATCAGTATATACACTTCAGATAACTACAC 126

Qy   164 TGAAGAAGTGGGGGTCTGAGACTATGACTCCAACAAGGAACCCTGCTTCGGGATGAAAA 223
            |||||||||||||||||||||||| ||||||||||||||
Db   127 CGGAGGAAATGGGGCTCAGGGGCTGCACTATGACTCCATGGAAGGAACCCTGTTTCCGTGAAGAAAA 186

Qy   224 CGTCCATTTCAATAGGATCTTCCTGCCCACCAATCTACTTCATCATCTTCTTGACTGGCAT 283
            ||||||  |||||||| |||| ||||||||||||||| |||||
Db   187 TGCTAATTCAATAAAATCTTCCTGCCCCACCAATCTACTCACTCCATCATCTTTAACTGGCAT 246

Qy   284 AGTCGGCAATGCAATGGTGATCATCTGGTCATGGGTTACCAGAAGAAGCTAAGGAGCATGAC 343
            ||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   247 TGTGGGCAATGAATGGTCTGTCATCCTGGTCATGGGTTACCAGAAGAAAACTGAGAAGCATGAC 306

Qy   344 GGACAAGTACCGGCTGCACCGTGCAGTGGCTGAGACTCTCTTTGTCATCACACTCCCCTT 403
            |||||||||||||||||||| ||||||||||||||||||||||||||
Db   307 GGACAAGTACAGGCTGCACCGTGCAGTGGCCGACTCTCTTTTGTCATCACACGCTTCCCTT 366

Qy   404 CTGGGCAGTTGATGGCCATGGCTGACTACTTTGGGGAAATTTTTGTGTAAGGCTGTCCA 463
            |||| |||||||||||| ||||||||||||||| |||||||||||||||||||
Db   367 CTGGGCAGTTGATGGCCCTGCAAATGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCA 426

Qy   464 TATCATCTACACTGTCAACCTGTCAGCAGCGCGTTCTCATCCTGGCCTTCATCCTGGCTGA 523
            |||||||||||||||||||| ||||||||||||||| |||||||||||||||||||||
Db   427 TGTCATCTACACACAGTCAACCTCTACAGCAGCGCGTTCTGCTCCATCCTGGCCTTCATCAGTCTGGA 486

Qy   524 CCGGTACCTCGCCATTGTCCACGGCCACCAACAGTCAAAGGCCAAGGAAACTGCTGGCTGA 583
            |||||||||| |||||| ||||||||||||||||||||||||||||||||
Db   487 CCGCTACCTCGCCATCGTCCACGCCACCAACAGTCAGAGGCCAAGGAAGCTGTTGGCTCGA 546

Qy   584 AAAGGCAGTCTATGTGGGGCGTCTGGCTGTGATCCCTGCTATACCTGACTTTCAT 643
            |||||||||| ||||||| ||||||| ||||||||||||||| ||||||||||
Db   547 AAAGGTGGTCTATGTTGGGGGTCTGCTGTGATCCCTGCTATTCCCGACTTCAT 606

Qy   644 CTTTGCCGACGCGTCAGCCAGGGGGGGACATCAGCGGGGGATGACAAGGTACAGTCATCTGACCG 703
            ||| ||||||||| |||||||||||||||||||||||||||||
Db   607 CTTTGCCAACG---------TCAGTGAGGCAGATGAAGTGACAGACAGATATATCTGTGACCG 651

Qy   704 CCTTTACCCCGATAGCCTGTGGATGGTGCGTGTTCAATTCCAGCATATAATGGTGGGTCT 763
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Db   652 CTTCTACCCCAATGACTTGTGGGGTGGTGTTGCCAGTTGCAGCATCATCATCTTCAGGTTGGCCT 711
            |||||||| ||||||| |||| ||||| ||||||||| |||| |||||||||| ||||||
Qy   764 CATCCTGCCCGGCATGTGCATCCTCGTGCTGTACACTGCATCATCATTATCATCTCAAGCTGTCACA 823
            |||||||| |||| ||||||||||| ||||| ||||||||||| |||||||||||||||
Db   712 TATCCTGCCTGGTATTGTCATCCTCGTGCTATTGCCATTATCATCTCCAAGCTGTCACA 771

Qy   824 CTCCAAGGCGCCACCAGACGCCAGGCGCCCAAGACGCACGACGCAGTCATCCTCATCCTCCTAGCTTT 883
            |||||||||||||||||||||||||||||| |||||||||||| ||||||||
Db   772 CTCCAAGGCGCCACCAGACGCAAGGCGCCCAAGACGCATCCTCATCCTCTGCTTT 831

Qy   884 CTTTGCCTGCTGGCTGCCATATATGTGGGATCAGCATGCGACTCGACTCCTTTGGG 943
            ||||||||||||||||||||||||||||||||||||||||| ||||||||
Db   832 CTTCGCCTGTTGGCTGCCTTACTACATTGGATCAGCATCAGCATCGACTCCTGA 891

Qy   944 AGTCATCAAGCAAGGATGTGACTTCGAGAGCATTGTGCACAAGCGGATCCTCCATCACAGA 1003
            |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db   892 AATCATCAAGCAAGGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTCCATCACCGA 951

Qy  1004 GGCCCTGCCTTCTTCCACTGTTGCCTGAACCCCATCCTCTATGCCTTCCTCGGGGCCAA 1063
            |||||||||||||||||||||||| ||||||||||||||||||||
Db   952 GGCCCTAGCTTCTTCCACTGTTGCTGAACCCCATCCTCTATGCTTTCCTTGGGAGCCAA 1011

Qy  1064 GTTCAAAAGCTCTGCCAGCCATGCCAGCACTCAACTCCATGAGCAGAGGCTCCAGCCTCCAAGAT 1123
            |||  ||| ||||||| |||||||||||| ||||||||||||||||||||||||
Db  1012 ATTTAAAACCTCTGCCCAGCCACCTCGTGAGCAGAGAGGTCCAGCCTCCAAGAT 1071

Qy  1124 CCTTTCCAAAGGAAAGCGGGGGTGGACACTTCTTCCGTCTCACTCGTTCCACTGAATCCTCCAG 1183
            |||||||||||||||||||||||||| |||||||||||||||||||
Db  1072 CCTCTCCAAAGGAAAGCGGAGTGGACATCATCGTTCCACTGAGTCTGAGTCTTCAAG 1131

Qy  1184 TTTTCACTCCAGCTAACCCTATGCAAAGACTTATATATATATATATATGATAAA 1243
            |||||||||||||||||| ||||||||||||||||
Db  1132 TTTTCACTCCAGCTAACACAGATGTAAAAGACTTTT------TTTATACGATAAATA 1183

Qy  1244 GAACTTTTTATGTTACACATTTCCAGATATAGAGACTGACCAGTCTCTGTACAGTTTT 1303
            ||||||||||| |||||||||||||||||||||| |||||||
Db  1184 ACTTTTTTTTAAGTTACACATTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTT 1243

Qy  1304 TTTTTTTTTTAATTGACTGTTGGGAGTTTATGTCCTCTAGTTTTTGTGAGGTTTGACT 1363
            ||||||||  ||||||||||| ||| ||||||||||| ||||
Db  1244 TATTGCTTGTTGGATTTTTGT-----CTTGTGTTTTTTTAGTTTTTTGTGAAGTTTAATT 1297

Qy  1364 TAATTTATATAAAATATTGTTTTTGTTCATGTGAATGAGCGTCTAGGCACGGACCT 1423
            ||||||||| ||||||||||||||||||||||||||| |||||
Db  1298 GACTTATTTATA----TAAATTTTTTGTTTCATATTGATGTGTTCATAGGCAGGACCT 1353

Qy  1424 GTGGCCAAGTCTTCTTAGTAGCTGTTTATCGTGTGTGTGAGAACTGTAGAGGAAGA 1483
            |||||||||||||||||||||| |||||||||||||||
Db  1354 GTGGCCAAGTTCTTAGTTGCTGTTGCTGTATGTCTCGTGGTAGGACTGTAGAA------AAGGG 1405

Qy  1484 AACTGAACATTCCAGAAATGTGTGTAAATTGAATAAAGCTAGCCGTGAATCCTCAGCTGTT 1543
            |||||||||||||||||||| ||| ||||| ||||||||||| ||||||||||||
Db  1406 AACTGAACATTCCAGAGGCGTGAGTGCTGTAGTGAAATGATCCCCAGCTGTT 1465

Qy  1544 GCTCGCATA 1551
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Db  1466 TATGCATA 1473
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RESULT 10
US-10-170-385-332
; Sequence 332, Application US/10170385
; Publication No. US2003020372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart

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; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 332
;   LENGTH: 1679
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-10-170-385-332
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Query Match           50.8%;   Score 952.8;  DB 6;  Length 1679;
Best Local Similarity 80.2%;   Pred. No. 2.8e-206;
Matches 1210;  Conservative  0;  Mismatches 252;  Indels  46;  Gaps  6;

Qy     44 GCAGGTGCGAGGTAGCAGTGACCCTCTGAGGCGTTTGGTGCTCCGGTAACCACCACGGCTG 103
          |||| ||||||||||||| |||   ||||||||| ||||| || ||||  ||||||||||
Db     12 GCGGCAGCAGGTAGCAAGTGACGCCGAGGGCCTGAGTGCTCCAGTAGCCACCGCATCTG 71

Qy    104 TAGAGCGAGTGTTGCCATGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTC 163
          ||  ||||||  ||||  ||||||||  ||||||||||||||||| ||||||||||||||
Db     72 GAGAACCAGCGGTTACCATGA----GGGGATCAGTATATATACACTTCAGATAACTACACAC 126

Qy    164 TGAAGAAGTGGGGTCTGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAA 223
          |||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    127 CGAGGAAAATGGGCTCAGGGGACTATGACTCATGAAGGAACCCTGTTTCCGTGAAGAAAA 186

Qy    224 CGTCCATTTCAATAGGATCTTCCTGCCCACCATCACTTCATCATCTTCTTGACTGGCAT 283
          |||||||||||||||  ||||||||||||||||||||||||||||| ||||||||||||
Db    187 TGCTAATTTCAATAAAATCTTCCTGCCCACCATCACTTCCTCATCTTCTTCAACTGGCAT 246

Qy    284 AGTCGGCAATGACTGGTGATCCTGGTCATGGGTTACCAGAAGAAGCTAAGGAGCATGAC 343
          ||  ||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Db    247 TGTCGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAAGAAACTGAGAAGCATGAC 306

Qy    344 GGACAAGTACCGGCTGCACCTGTCAGTGGCTGACCCTCCTTGTCATCACACTCCCCTT 403
          ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    307 GGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCCTCCTCTTTGTCATCACGCTTCCCTT 366

Qy    404 CTGGGCAGTTGATGCCATGGCCATGTGACTGGTACTTTGTGGTAAGGCTGTCCA 463
          ||||||||||||||||||||||||||||||||||||  |||||||||||||||||
Db    367 CTGGGCAGTTGATGCCGGTCTGGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCA 426

Qy    464 TATCATCTCACACTGTCAACCTCTACAGCACGCGTTCTCATCCTGCCCTTCATCAGCCTGA 523
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 TGTCATCATCCACAGTCAACCTCTACAGCACGCGTCCTCATCCTGCCCTTCATCAGTCGCTGGA 486

Qy    524 CCGGTACCTCGCCATTGTCCACGCGCCACCAACAGTCAAAGGCCAAGGAAACTGCTGGCTGA 583
          |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db    487 CCGCTACCTCGCCATCGTCCACGCGTCCACCAACAGTCGGCGGCCAAGGAAGCTGTTGGCTGA 546

Qy    584 AAAGGCAGTCTATGTGGGGCGTCTGGATCCAGCCCTCCTCCTGCTAGTACCTGACTTCAT 643
          |||||||||||||||||||||||||||||||||||||||||||||||  |||||||||
Db    547 AAAGGTGGTCTATGTTGGGCGTCTGGATCCGATCCCGCCCCTCCTGCTAGTACCTGACTTCAT 606

Qy    644 CTTTGCCGACGTCAGCCAGGGGACATCAGTGGGGATGACAGGTACATCTGTGACCG 703
          |||||||||||||||||||     ||||||||||||||||||||||||||||||||
Db    607 CTTTGCCAACG-------TCAGTGAGCGAGTGACAGGTTGACAGATATATCGTGTGAACCG 651

Qy    704 CCTTTACCCGATAGCCTGTGGATGGTGGTGTGTTCAATTCCAGCATAATAAGTGTGGGGTCT 763
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    652 CTTCTACCCCCAATGACTTGTGGGTGTTGTGTGTTCCAGTTTCAGCACCATGGTTGGCCT 711

Qy    764 CATCCTGCCCGGCCATCGTCATCCTCTCCTGTTACTGACATCATCATCTTCAAGTGTCACA 823
          ||||||||  |||||||||||||||||||||||||| ||||||||||| ||||||||||||
Db    712 TATCCTGCCTGGGTATTGTCATCCTGCTCCTGCTATTGCATTATCATCTCCAAGCTGTCACA 771

Qy    824 CTCCAAGGGGCCACCAGGAAGGCGCAAGGCCTCAAGACGACGCAGCAGTCATCATCCTCAGCTTT 883
          ||||||||||||||||||||||||||||||||||||| |||||||||||||||  |||| ||||
Db    772 CTTTGCCTGGCTGCCATTATGGGGATCCAAGAAGGCGCAAGGCCTCAAGACTCATCCTCATCCTGGCTTT 831

Qy    884 CTTTGCTGCTGGCTGCCATTATGTGGGATCAGCATTGTGCACAAGTGACTGACACTCCTTTTGGG 943
          |||||||||  |||  |||||||||||||||||||  ||||||||||||||||||  ||||
Db    832 CTTTGCGCTGTTGGCTGCCTTACTACATGGGATCAGCATCAGCATCGACTGACTCCTCCTGGA 891

Qy    944 AGTCATCAAGCAAGGATGTGACTTGGAGAGCATTGTGCACAAGTGACTCCATCACAGA 1003
          |||||||||||||||||||||  |||||||  |||||||||||||||||||||||||
Db    892 AATCATCAAGCAAGGGTGTGAGTTTGAGACACTGTGACAAGTGGATTTCCATCACCGA 951

Qy   1004 GGCCCTGCCTTCTTCCACTGTTGCCTGAACCCATCCTCATGAGCTTCCTCGGGGCCAA 1063
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    952 GGCCCTAGCTTCTTCCACTGTTGTCTGAACCCCATCCTCATGTCTTCATGTCCTTGGAGCCAA 1011

Qy   1064 GTTCAAAAGCTCTGCCCAGCATGCACTCAACTCACTCTCCCGTCTCCAGCCTCAAGAT 1123
          |||||||| ||||||||||||||||||  || |||||||||| |||||||||||||
Db   1012 ATTTAAAACCTTCTGCCCAGCACGCGACTCGTGAGCAGAGGGTCCAGCCTCAAGAT 1071

Qy   1124 CCTTTCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGAATCCTCCAG 1183
          |||||||||||||||||||  |||||||||||||| |||||||| |||||||||||||||
Db   1072 CCTCTCCAAAGGAAAGCGAGGTGGGACATTCATCTGTTTCCACTGAGTCTGAGTCTTCAAG 1131

Qy   1184 TTTTCACTCCAGCTAACCCTTATGCAAAGACTTATATAATATATATATATATATGATAAA 1243
          |||||||||||||||||||||||||||||||||||||||||      ||||||||||||
Db   1132 TTTTCACTCCAGCTAACACAGATGTAAAAGACTTTTT------TTTATACGATAAATA 1183

Qy   1244 GAACTTTTTATGTTACACATTTCCAGATATAAGAGACTGACCAGTCTTGTACAGTTTT 1303
          ||||||||  ||||||||||||||||||||||  |||||||||||  |||||||||
Db   1184 ACTTTTTTTAAGTTACACATTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTT 1243

Qy   1304 TTTTTTTTTTTTAATTGACTGTGGAGGTTTATGTTCCTCTAGTTTTGTGAGGTTTGACT 1363
          |||||   |||||||||||||    ||   |||||||||  |||||||||||||| |||
Db   1244 TATTGCTTGTTGGATTTTTGT------CTTGTGTTTTGTTTTAGTTTTGTGAAGTTTAATT 1297

Qy   1364 TAATTTATATAAATATTGTTTTTGTTCATGTGAATGAGTCTCAGGCAGGACCT 1423
          |||||||||     ||||||| |||||||||||||||||||||||  ||||||||
Db   1298 GACTTATTTATA----TAAATTTTTTGTTCATTTGATTGTGTGTCAGGCAGGACCT 1353

Qy   1424 GTGGGCCAAGTTCTTAGTAGCTTTTATCTGTGTTATCTGTGTAGAACTGTGTAGAGGAAGA 1483
          ||||||||||||||||||||||    |||||||||||||| ||||||||||||||
Db   1354 GTGGGCCAAGTTCTTAGTTGCTGTTATGTGTGTATGCTCTCGTGGTAGGACTGTAGAA-------AAGGG 1405

Qy   1484 AACTGAACATTCCAGAATGTGTGGTAAATGAATAAAGCTAGCCGTGATCCTCAGCTGTT 1543
          ||||||||||||||||||||||||  |||||||||||||||||||||||||| |||||
Db   1406 AACTGAACATTCCAGAGCCGTGAGTTGGAATCACGTAAAGCTAGAAAATGATCCCCAGCTGTT 1465

Qy   1544 GCTGCATA 1551
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Db   1466 TATGCATA 1473
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RESULT 11
US-10-341-434-177
; Sequence 177, Application US/10341434
; Publication No. US20030215835A1
; GENERAL INFORMATION:
; APPLICANT: OriGene Technologies
; TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
; FILE REFERENCE: 9U 204 205 R1
; CURRENT APPLICATION NUMBER: US/10/341,434
; CURRENT FILING DATE:  2003-07-18
; PRIOR APPLICATION NUMBER: US 60/348,164
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/348,119
; PRIOR FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 177
;   LENGTH: 1679
;   TYPE: DNA
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;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (89)..(1144)
;  OTHER INFORMATION:
US-10-341-434-177

Query Match     50.8%;  Score 952.8;  DB 6;  Length 1679;
Best Local Similarity  80.2%;  Pred. No. 2.8e-206;
Matches 1210;  Conservative  0;  Mismatches 252;  Indels  46;  Gaps   6;

Qy   44 GCAGGTGCAGTAGCAGTGACCCTGCAGCCGGTTTGGTGCTCCCGGTAACCACCACGGCTG  103
         |||||| |||||  ||| ||||| |||| |  ||| ||||| || | ||||||| | ||||
Db   12 GCGGCAGCAGGTAGCAAAGTGACGCCGAGGGGCCTGAGTGCTCCAGTGCCACCGCATCTG   71

Qy  104 TAGAGCGGAGTGTTGCCATGGAACCGATCAGTGTGAGTATATACACTTCGATAACTACTC  163
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Db   72 GAGAACCAGCGGTTACCATGGA----GGGGATCCAGTATATACACTTCAGATAACTACAC  126

Qy  164 TGAAGAAGTGGGGTCTGGAGACTATGACTCCAACAACAAGAACCCTGCTTCCGGGATGAAA  223
         | ||||| |||||| | || ||| |  |   ||  |||  |||||||| |||||| |||||
Db  127 CGAGGAAATGGGGCTCAGGGGACTCCATGAAGGACCCTGTTTCCGGTGAAGAAAA       186

Qy  224 CGTCCATTTCAATAGGATCTTCCTGCCCACCACCATCCTTCATCCTCTTCTTGACTGGCAT  283
         |||| |||||||||  ||||||||||||||| |  || |||| |||||| || ||||||||
Db  187 TGCTAATTTCAATAAAATCTTCCTGCCCACCATCCTCCTACTCCATCATCTTCTTAACTGGCAT  246

Qy  284 AGTCGGCAATGGATTGGTGATCCTGGTCATGGGTACCAGAAGAAGCTAAGGAGCATGAC  343
         | | ||||||||||||||| |||||||||||||||||||| ||||| |||||||||||||
Db  247 TGTGGGCAATGGATTGGTCATCCTGGTCATGGGTACCAGAGAAACTGAGAAGCATGAC  306

Qy  344 GGACAAGTACCGGCTGCACCTGTCAGTGGCTGCCGACCTCCTTGTCATCACACTCCCCTT  403
         |||||||||| ||||||||||||||||| | |||||||||||| || |||| || ||||
Db  307 GGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTCCTTGTCATCACGCTTCCCTT  366

Qy  404 CTGGGCAGTTGATGCCATGGCTGCTCAGTGTCATGGCTACTTTGGGGAAATTTTGTGTAAGGCTGTCCA  463
         ||||||||||||||||| | |  | |||| ||| |||||||||||  |||||||||||| ||||||| |
Db  367 CTGGGCAGTTGATGCCAGTGCCGTGCAGTTGTACTTTGGGCAAACTTTCCATGCCTTCATCCTGCCCATCCTGCTCAGTCTGGA  426

Qy  464 TATCATCTACACTGTCAACCTCTACAGCAGCGTGTTCTCATCCTGGCCTTCATCAGCCTGA  523
         ||||||||||| |||||  |||||||||||||||| |||||| |||||||||||| |||||
Db  427 TGTCATCTACACAGTCAACCTCTACAGCAGCGTGTCCTTCATCCGGCCCTTCATCAGCTGA  486

Qy  524 CCGGTACCTCGCCATTGTCCACGGCACCACCAACAGTCAAGGAAACTGCTGGCTGA  583
         || || ||| || |||||||| || || ||||||||| ||||||| ||||||||
Db  487 CCGCTACCTGGGGCCATCGTCCACGGCACCACCAACAGTCCAAGGAAGCTGTTGGCCTGA  546

Qy  584 AAAGGCAGTCTATGTGGGCCGTCTGGATCCCAGCCCTCCTGGACTATACCTGACTTCAT  643
         |||||| ||||||||||| | |||||||||||||||||||||||| | | ||||||||||
Db  547 AAAGGTGTCTATGTTGGGCCGTCTGGATCCCAGCCCTCCTGCTGATTCCCGACTTCAT  606

Qy  644 CTTTGCCGACGCTCAGCCAGGGAGCGTACCAAGGGGACAATCAGTGACAGGGTACATCTGTGACCG  703
         |||||||||||| ||||||||| |  | |   |  |||||| || || || | ||||||||||||||
Db  607 CTTTGCCAACG--------TCAGTGAGGCAGATGACGACATATCTGACCG  651

Qy  704 CCTTTACCCCGATAGCCTGTGGATGGTGGTGTTTCAAATTCCAGCATAAATGGTGGGGTCT  763
         || |||||||||| |||| |||| || |||| | | |||||||| ||| |||||||| | |
Db  652 CTTCTACCCCAATGACTTGTGGGCGGTTGTGTTTCCAGTTTCAGCGTTTGGGCATATGTGGCCT  711

Qy  764 CATCCTTGCCCGGCATCATCGTCATCATCATCCTGTTACTGCATCAATCATCTTCCTTAAGCTGTCACA  823
         ||| | ||||| |||||| |||||||||| | |  | |||| || |||| || |||| | |||||||||
Db  712 TATCCTTGCCCGGTATTGTCATCATCATCTGCATTATTGCATCAGTCATCTTCCTCAGCTGTCACA  771

Qy  824 CTCCAAGGGCCACCAGAAGCGCAAGGGGATGAGCAGTACATCTGTGACCGT  883
         |||||||||||| ||||||| || ||||||||| | || |||| |||||||||
Db  772 CTCCAAGGGCCACCAGAAGCGCAAGGGCCTCAAGACACCAGTATATCGTGACCG  831

Qy  884 CTTTGCCGCTGCCCATTATGTGGGGATCCGCCATATTATGTGGGGGATCTTTTTGGG  943
         || |||||| |||||  ||||| || | |||||||| |||  |||| ||||||||||
Db  832 CTTCGCCCCTGTTGGCCTACTCATTGGGATCAGCACTACTGGGATCATCCTTCTGA  891

Qy  944 AGTCATCATCAAGCAAGGACGGATGGACTTCGAGAGACATTGTGCACAAGTGGGATCTCCATCACAGA 1003
         | ||||||||||||||||||||||||||||||||||||||||||||
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Db  892 AATCATCAAGCAAGGTGTGTGAGTTTGAGAACACTGTGCACAAGTGGATTTCCATCACCGA  951

Qy 1004 GGCCCTGCCTCTTCCACTGTTGCCTGCTGACCCATCCTCCTCTGCCTTCCTTCGGGGCCAA 1063
         |||||| | || ||||| |||||| || | | |||||||||| | || | ||||||| ||||
Db  952 GGCCCTAGCTTCTTCCACTGTTGTCTGAACCCCATCCCCATCTTCCTTATGTCTTTCCTTGGAGCCAA 1011

Qy 1064 GTTCAAAAGCTCTGCCCCAGCATGCATGACCCTCAACTCAACTCCATGAGCAGAGGCTCCAAGAT 1123
         ||||||||||  |  ||||| | ||| ||||| |||||||||||  ||||||||| |||||||||||
Db 1012 ATTTAAAACCTCTGCCCCAGCACGCATCACCCTCCACCTGTGAGCAGCAGAGGGTCCAGCCTCCAAGAT 1071

Qy 1124 CCTTTCCAAAGGAAGACGCGGGTGGACACACTCTTCCGTCTCCACGGAGTCAGAATCCTCCAG 1183
         | || |||||||||| | |  | || || |||||||| |||||||| |||| ||||| ||||
Db 1072 CCTCTCCAAAGGAAGGAGGCGGTGGAGCATTCATCTGTTTCCACTGAGTCTCGTCAAG 1131

Qy 1184 TTTTCACTCCAGCTAACCCTATGCAAGACTAATATATATATATAATGATAAA 1243
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Db 1132 TTTTCACTCCAGCTAACACAGATGTAAAAGACTTTTT-------TTTATACGATAAATA 1183

Qy 1244 GAACTTTTTATGTTACACATTTTCCAGATATAAGACTGACCAGTCTTGTACAGTTTT 1303
         ||| ||||||| ||||||||||||||||||| ||| || ||| |||| |||||||||
Db 1184 ACTTTTTTTTAAGTTACACATTTTCAGATATAAAAAGACTGACCAATATTGTACAGTTTT 1243

Qy 1304 TTTTTTTTTTAATTGACTGTGTGGGGAGTTTATGTTCCTCTAGTTTTGTGAGGTTTGACT 1363
         ||| | |  |||    |||||||||| | |  |||||||   |  || | | ||||||| |
Db 1244 TATTGCTTGTTGGATTTTGT------CTTGTGTTTCTTTAGTTTTGTGTGAAGTTTAATT 1297

Qy 1364 TAATTTATATAAATATTGTTTTTTGTTCGTTCATGTGAATGAGCGTCTAGGCAGGACCT 1423
         ||||| ||| | |  |||||| ||||   | |||||   ||| |||||
Db 1298 GACTTATTTATA----TAAATTTTTTGTTTTTCATATTGATGTGTCTGAGGCAGGACCT 1353

Qy 1424 GTGGCCAAGTCTTAGTAGCTGTTTATCTGTGTGGAGGACTGTAGAAACTGTAGAGGAGA 1483
         |||||||||||||||||||||  |  | ||||| |||||  |  |  || |||   ||-------AAGGG 1405
Db 1354 GTGGCCAAGTCTTAGTTGCTGTATGTCGTGTATGTGGTAGGAACTGTAGAA--------AAGGG 1405

Qy 1484 AACTGAACATTCAGAAATGTGTGTAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTT 1543
         ||||||||||||||||| || |||| |||| | ||| | ||| | |  | | |||||||
Db 1406 AACTGAACATTCCAGAGCGGTGTAGTGAATCACGTAAAGCTAGAAATGATCCCAGCTGTT 1465

Qy 1544 GCTGCATA 1551
         ||||||||
Db 1466 TATGCATA 1473
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Query Match   50.8%; Score 952.8; DB 6; Length 1679;

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Best Local Similarity  80.2%;   Pred. No. 2.8e-206;
Matches 1210;  Conservative  0;  Mismatches 252;  Indels  46;  Gaps  6;

Qy    44  GCAGGTGCAGGTAGCAGTGACCCTCTGAGCGTTTGGTGCTTCCGGTAACCACCACGGCTG  103
          ||| ||||| |||||| ||||||||||| |||||||| |||||||||||||||||||||||
Db    12  GCGGCAGCAGGTAGCAAAGTGACGCCGAGGGCCTGAGTGCTCCAGTAGCCACCGCATCTG  71

Qy   104  TAGAGCGAGTGTTGCCATGGAACGATCAGTGTGAGTATATACACTTCTGATAACTACTC  163
          ||||    |||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    72  GAGAACCAGCGGTTACCATGGA-----GGGATCAGTATATACACTTCAGATAACTACAC  126

Qy   164  TGAAGAAGTGGGGTCTGAGACATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAA  223
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   127  CGAGAAAATGGGCTCAGGGACCATATGACTCCATGAAGAGAACCCTGTTTCCGTGAAGAAAA  186

Qy   224  CGTCCATTTCAATAGGATCTTCCTGCCCACCATCTACTTCATCATCTCTGACTGGCAT  283
          |||| ||||||||   ||||||||||||||||||||||||||||||||||||||||||||
Db   187  TGCTAATTTCAATAAAATCTTCCTGCCCACCATCTACTTCATCATCTTCTTAACTGGCAT  246

Qy   284  AGTCGGCAATGGATGGTGATCCTGGTCATGGGTTACCAGAAGAAGCTAAGGAGGCATGAC  343
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   247  TGTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAAGAAACTGAGAAGCATGAC  306

Qy   344  GGACAAGTACCGGCTGCACCTGTCAGTGGCTGACTCCTCTCTTGTCATCACACTTCCCCTT  403
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db   307  GGACAAGTACAGGCTGCACCTGTCAGTGGCCGACTCCTCCTTGTCATCATCTTTGTCTCCTT  366

Qy   404  CTGGGCAGTTGATGCCATGGCTGACTGGTACTTTGTGTTGAAATTTTTGTGTTAAGGCTGTCA  463
          |||||||||| || |||||||||||||||||||||||||||||||||||||||||||||
Db   367  CTGGGCAGTTGATGCCGTGGCTGCAAACTGGTACTTTGGGAACTTCCTATGCAAGGACAGTCCA  426

Qy   464  TATCATCATCTACACTGTCAACCTTCTACAGACGCGTCTCATCTGGCCTTCATCAGCCTGA  523
          ||||||||||||||||||| ||||||||||||||||||||||||  ||||||||||||||
Db   427  TGTCATCATCACAGTCAACCTCTACACCCTACAGACGTCCTCATCTGGCCTTCATCAGTCTGA  486

Qy   524  CCGGTACCTCGCCATTGTCCACGCCACCAACAGTCAAAGCCAAGGAAACTGCTGGCTGA  583
          |||| ||||| |||  ||||||||||||||||||||||||||||||||||||||||||||
Db   487  CCGCTACCTGGCCATCGTCCAGCGCCACCAACAGTCAGAGGAAGGAGCTGTGTTGGCTGA  546

Qy   584  AAAGGCAGTCTATGTGGGGATCTGAGGATCCCAGCCTCCTCCTGACTATACCTGACTTCAT  643
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   547  AAAGGTGGTCTATGTGGGGGTCTGAGATCCCGTCCCTCCGTCTGACTATTCCCGACTTCAT  606

Qy   644  CTTTGCCGACGTGCAGCGTCAGCGCCAGGGGGACATCAGTCAGGGGGATGACAGGTACACATCTGTGACCG  703
          ||||||| |||| ||                    |||||||||||||||||||||||||||
Db   607  CTTTGCCAACG------------------------TCAGTGAGGCAGATGACAGATATATCTGTGACCG  651

Qy   704  CCCTTACCCCGATAGCCTGTGGATAGTGGTCTGGTTGTTTCAATTCCAGCATATATAATGGTGGGTCT  763
          | ||| ||||  |||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db   652  CTTCTACCCCAATGACTGTGGGGTGTGGTTGGTTGTGTTGCCAGTTTCAGCACATCATGTTGGGCCT  711

Qy   764  CATCCTGCCCGGCGATCGTCATCGTCTCCTGTTACTGACATCATCATCTCTAAGCTGTCACA  823
          ||||||||||| |||||||||||||||||||||||||| ||||||||||||||||||||||
Db   712  TATCCTGCCTGGTATTGTCATCGTCTCCTGCTATTGTGACATTGTATCATCCTCAAGCTGTCACA  771

Qy   824  CTCCAAGGGCCACCAGAGCGCCAAGAGCGCCAGAGTCTCAGACGACAGTCATCATCCTAGCTTT  883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   772  CTCCAAGGGGCCACCAGAAGCGCCAAGAGCCACCAGTGCATCTCATCATCCTCGGCTTT  831

Qy   884  CTTTGCCTGGCTGCCCATATATGTGGGATCAGCATCAGCGACTCCTTTCATCCTTTTGGG  943
          ||| |||| |||| |||||||||||||||||||||||||||||||||||||||||||||
Db   832  CTTCGCCTGTGTTGGCTGCCTTACTACATTGGATCAGCATCGGATCAGCGACTCCTTCATCCTCTGA  891

Qy   944  AGTGTCATCAAGCAAGGATGGATGGCATTGTCAGAGCAGCATTGTGCACAAGGTGGATCTCCATCACAGA  1003
          ||| ||||||||||||||||  ||||||||||||||||||||||| ||| |||||||||
Db   892  AATCATCAAGCAAGGTGAGTTTGAGAACACTGTGAGACAGTGGATTTCCATCACCGA  951

Qy  1004  GGCCCTCGCCTTCTGCCTTCTTCTTCCCACTGTTGCCTGGTGATCCTCTCTATGCCTTCCTCGGGGGCCAA  1063
          ||| ||||||||||||| |||||||| |||||||||||||||||||||||||||||||||||
Db   952  GGCCCTCAGCTTTCTTCTTCCTCCACTGTGTCTGGAAGCCAAGCTGGGAGGCCAA  1011

Qy  1064  GTTCAAAAGCTCTGCCCAGCATCGACTCAACTCCATGAGCAGAGGCCTCCAGCCTCAAGAT  1123
          || |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
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Db  1012  ATTTAAAACCTCTGCCCAGCACGCACTCACCTCTGTGAGCAGAGGGTCCAGCCTCAAGAT  1071

Qy  1124  CCTTTCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGAATCCTCCAG  1183
          ||||| |||||||||||| |||||||||| |||||||||||||||||||||||||
Db  1072  CCTCTCCAAAGGAAAGCGAGTGGACATTCATCCGTCTTCCACTGAGTCTGAGTCTTCAAG  1131

Qy  1184  TTTTCACTCCAGCTAACCCTTATGCAAAGACTTATATAATAATATATATGATAAA  1243
          |||||||||||||||||||||||||||||||||       --TTTATACGTATAAATA
Db  1132  TTTTCACTCCAGCTAACACAGATGTAAAGACTTTTT--------TTTATACGTATAAATA  1183

Qy  1244  GAACTTTTTATGTTACACATTTCCAGATATAAGAGACTGACCAGTCTTGTACAGTTTT  1303
          ||||||||||||||| |||||||||||||||| || |||||| |||||||| ||||||
Db  1184  ACTTTTTTTTAAGTTACACATTTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTT  1243

Qy  1304  TTTTTTTTTTAATTGACTGTTGGGAGTTTATGTTCCTCTAGTTTTTGTGAGGTTTGACT  1363
          | ||||  ||||||||||||| ||    |||||||||||  ||||||||||||||  ||||
Db  1244  TATTGCTTGTTGGATTTTTGT-----CTTGTGTTTCTTTAGTTTTTGTGAAGTTTAATT  1297

Qy  1364  TAATTTATATAAATATTGTTTTTTGTTGTTTTCATGTGAATGAGCGTCTAGGCAGCAGGACCT  1423
          |||||||  ||| |||||||||||| | ||| ||||||||||||||||||||||
Db  1298  GACTTATTTATA----TAAATTTTTTTGTTCATATTGATGTGTGTCTAGGCAGGACCT  1353

Qy  1424  GTGGCCAAGTTCTTAGTAGCTGTTATCTGTGTAGGACTGTAGAACTGTGAGAGGAAGA  1483
          ||||||||||||||||||||||||||||||||      --AAGGG
Db   1354  GTGGCCAAGTTCTTAGTTGCTGTGTATGTCTCGTGGTAGGACTGTAGAA--------AAGGG  1405

Qy  1484  AACTGAACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTT  1543
          ||||||||||||||||||||||| |||| |||| |||||||||||||||||||||||||
Db   1406  AACTGAACATTCCAGAGCGTGTAGTGAATCACGTAGTGGTAGAAATGATCCCCAGCTGTT  1465

Qy  1544  GCTGCATA  1551
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Db   1466  TATGCATA  1473
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RESULT 13
US-10-211-462-80
; Sequence 80, Application US/10211462
; Publication No. US20040033495A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynne, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators
; FILE REFERENCE: 018501-006200US
; CURRENT APPLICATION NUMBER: US/10/211,462
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/791,390
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: US 60/310,025
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/334,244
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-462-80

Query Match   50.8%;   Score 952.8;   DB 7;   Length 1679;
Best Local Similarity 80.2%;   Pred. No. 2.8e-206;
Matches 1210; Conservative 0; Mismatches 252;   Indels 46;   Gaps   6;

Qy   44 GCAGGTGCAGGTAGCAGTGACCCTCTGAGCGTTTGGTGCTTCCGGTAACCACCACGGCTG 103
          ||| ||||| |||||| ||||||||||| |||||||| |||||||||||||||||||||||
Db   12 GCGGCAGCAGGTAGCAAAGTGACGCCGAGGGCCTGAGTGCTCCAGTAGCCACCGCATCTG 71

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Qy   1184  TTTTCACTCCAGCTAACCCTTATGCAAAGACTTATATATATATATATATATATATATGATAAA  1243
           |||||||||||||||||||||||||||||||||||||     |||           ||||||
Db   1132  TTTTCACTCCAGCTAACCAGCAGATGTAAAAGACTTTT------TTTATACGATAAATA      1183

Qy   1244  GAACTTTTTTATGTTACACATTTTCCAGATATAAGAGACTGACCAGTCTTGTACAGTTTT  1303
           |||||||||  |  |||||||||||||  |||||||||||||||||||||||||||||
Db   1184  ACTTTTTTTTAAGTTACACATTTTCAGATATAAAAGACTGACCAATATTGTACAGTTTT  1243

Qy   1304  TTTTTTTTTAATTGACTGTTGGGAGTTTATGTTCCTCCTCCAGTTTTGTGAGGTTTGACT  1363
           |       |||||||  |||||||         |||||||||||||||||||||||
Db   1244  TATTGCTTGTGTGGATTTTTGT------CTTGTGTTCTTTAGTTTTTGTGAAGTTTAATT  1297

Qy   1364  TAATTTATATAAATATTGTTTTTGTTTTGTTCATGTGAATGAGCGTCAGCAGGACCT  1423
           |   ||||||||| |  ||||||||||||||||||||||||||||||||||||||||
Db   1298  GACTTATTATTA----TAAATTTTTTTGTTTCATATTGATGTGTGTCAGGCAGGACCT  1353

Qy   1424  GTGGCCAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTAGAACTGTAGAGGAAGA  1483
           |||||||||||||||||||||||||||||||||||||||||||||||       |||||
Db   1354  GTGGGCCAAGTTCTTAGTTGCTGTGTATGTCTCGTGGTAGGACTGTAGAA------AAGGG  1405

Qy   1484  AACTGAACATTCCAGAATGTGTGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTT  1543
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1406  AACTGAACATTCCAGAGCGTGTAGTGAATCACGTAAAGCTAGAAATGATCCCCAGCTGTT  1465

Qy   1544  GCTGCATA  1551
           ||||||||
Db   1466  TATGCATA  1473
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RESULT 14
US-10-181-906-9
; Sequence 9, Application US/10181906
; Publication No. US20040053864A1
; GENERAL INFORMATION:
; APPLICANT: Karsenty, Gerard
; APPLICANT: Amling, Michael
; APPLICANT: Ducy, Patricia
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROL OF BONE FORMATION VIA
; TITLE OF INVENTION: MODULATION OF NEUROPEPTIDE Y ACTIVITY
; FILE REFERENCE: 9142-020-999
; CURRENT APPLICATION NUMBER: US/10/181,906
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/02040
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-181-906-9

Query Match   50.8%; Score 952.8; DB 7; Length 1679;
Best Local Similarity   80.2%; Pred. No. 2.8e-206;
Matches 1210; Conservative   0; Mismatches 252; Indels 46; Gaps   6;

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Qy    44  GCAGGTGCAGGTAGCAGTGACACCCTCGAGGCGTTGGTGCTCCGTAACCACCACGGCTG  103
          ||  ||||||||  ||||||||||||||   ||||||| |||||||||   ||||||||
Db    12  GCGGGCAGCAGGTAGCAGAGTGACCGCCGAGCGGGCCTCCAGTAGCGACCACCGCATCTG   71

Qy   104  TAGAGCGAGTGTTGCCATGGAACCATCAGTGTGAGTATATACACTTCTGATAACTACTC  163
          ||  |||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db    72  GAGAACCAGCGGTTACCATGGA------GGGGATCAGTAGTATATACACTTCAGATAACTACAC  126

Qy   164  TGAAGAAGTGGGGTCTGGAGACTATGACTCCAACAAGGAACCCTGCTCCGGGATGAAAA  223
          ||   ||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db   127  CGAGGAAATGGGCTCAGGGGACTATGACTCCATGGGGGACTCCATGAGGAACCCTGTTCCGTGGAAGAAAA  186

Qy   224  CGTCCATTCAATAGGATCTTCCTGCCACCACCATCTCATCATCCATCCATCCATCTTGACTGGCAT  283
          | |||||| |||||  ||||||||||||||||||||||||||||||||||||||||
Db   187  TGCTAATTTCAATAAAATCTTCCTGCCACCACCATCATCTTCTTAACTGGCAT  246

Qy   284  AGTCGGCAATGGATTGGTGATCCTGGTCATGGGTTACCAGAGAAGCTAAGGAGGCATGAC  343
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   247  TGTGGGCAATGGATTGGTCATCCTGGTCATGGGTTACCAGAGGAAAACTGAGAAGCATGAC  306

Qy   344  GGACAAGTACCGGCTGCACCTGTCAGTGGCTGACCTGCTTGTCATCACACTTCCCCTT  403
          |||||||||||||||||||||||||||||||||||||||||  |||| |||||||||
Db   307  GGACAAGTACAGGCTGCACCTGTCAGTGGCCGACCTGCTTGTCATCACGCTTCCCTT  366

Qy   404  CTGGGCAGTTGATGCCATGGCTGACTTGGTACTTTGGGGAAATTTTTGTGTAAGGCTGTCCA  463
          ||||||||  |||||||||||||||||||||||||||  ||||||||||||||||||||
Db   367  CTGGGCAGTTGATGCCGTGTGCAAACTGGTACTTTGGGGAACTTCCTATGCAAGGCAGTCCA  426

Qy   464  TATCATCTACACTGTCAACCTCTACAGAGCGGTTCTCATCCTGCCTTCATCAGCCTGA  523
          ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||
Db   427  TGTCATCTACACAGTCAACCTCTACAGAGCGGTCCTCATCCTGCCTTCATCAGTCTGA  486

Qy   524  CCGGTACCTCGCCATTGTCCACGCCACCACAAGTCAAAGGCAAGGAAAACTGCTGGCTGA  583
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   487  CCGCTACCTGGCCATCGTCCACGCCACCACCAACAGTCAGAGGCAAGGAAGCGAAGCTGTTGGCTGA  546

Qy   584  AAAGGCAGTCTATGTGGGGCGTCTGATCCAGCCCTCCTCTGCACTATACCTGACTTCAT  643
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   547  AAACGTGGTCTATGTGGGGCGTCTGGATCCCTCCTCTGCACTATTCCCGACTTCAT  606

Qy   644  CTTTGCCGACGTCAGCCAGGGGACATCAGTCAGGGGGATGACAGGTACATCTGTGACCG  703
          |||||||||||||||        |||||||||||||||||||||||||||||||||||
Db   607  CTTTGCCAACG--------TCAGTGAGGCAGATGACAGATATATCTGTGACCG  651

Qy   704  CCTTACCCCGATAGCCTGTGGATGGTGATTCAATTCCAGCATATAATGGTGGTCT  763
          | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   652  CTTCTACCCCAATGACTTGTGGGGTGTTGTGTCCAGTTTCAGCACATCATGGGCCT  711

Qy   764  CATCGTGCCCGGCCGACATCGTCATCCTCCTCGTTACTGCATCATCATCATCTCAAGCTGTCACA  823
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   712  TATCCTGCCTGGTATTGTCATCCTGTCTATTGCATTGCATTATCATCTCCAAGCTGTCACA  771

Qy   824  CTCCAAGGGCCACCAGAAGCGCAAGAGCGCAAGGCCCTCAAGACGACCAGTCATCCTCATCCTCTAGCTTT  883
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   772  CTCCAAGGGCCACCAGAAGCGCAAGGCGCCTCAAGAGCACCACAGTCATCCTCATCCTCTGGCTTT  831

Qy   884  CTTTGCCTGCTGGGCTGCCCCATATATGTGGGGATCAGCATCAGCAGCATCGACTCCTTCATCATCCTTTGGG  943
          |||||||||||||||||||||| ||  ||||||||  ||||||||||||||||||||
Db   832  CTTCGCCTGTGTGGCTGCCTTACTACATTGGGATCAGCATCAGCAGCATCGACTCCTTCATCATCCTTGA  891

Qy   944  AGTCATCAAGCAAGGATGTGACTTCGAGAGCATTGTGCACAAGTGATCTCCATCACAGA  1003
          |||||||||||||||||||||| |||||||||  ||||||||||||||||||||||||
Db   892  AATCATCAAGCAAGGATGTGAGTTTGAGAAACACTGTGCACAAGTGGATTTCCATCACCGA  951

Qy  1004  GGGCCCTCGCCTTCTTCCACTGTTGCCTGAACCCATCCTCCTATGCCTTCCTCTCGGGGCCAA  1063
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   952  GGGCCTAGCTTTTCTTCCACTGTTGTCTGAACCCCATCCTCTATGCTTTCCTATGCTTTGGAGCCAA  1011

Qy  1064  GTTCAAAAGCTTGCTCCGCCAGCACTCAACTCATGAGGCAGAGGCTTCCAGCCTCAAGAT  1123
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1012  ATTTAAAACCTTGCCCAGCACCGCACCTCGTGAGCGAGGGGTCCAGCCTCAAGAT  1071

Qy  1124  CCTTTCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCAGGAGTCAGAATCCTCCAG  1183
          ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db  1072  CCCTTCCAAAGGAAAGCGAAGGCGAGGTGGACATTCATCTGTTTCCACTGAGTCTTCAAG  1131

Qy   284  AGTCGGCAATGGATTGGTGATCCTGGTCATGGGTTACCAGAGAAGCTAAGGAGGCATGAC  343
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RESULT 15
US-10-342-887-912
; Sequence 912, Application US/10342887
; Publication No. US2004005834OA1
; GENERAL INFORMATION:
;   APPLICANT: Dai, Hongyue
;   APPLICANT: He, Yudong
;   APPLICANT: Linsley, Peter S.
;   APPLICANT: Mao, Mao
;   APPLICANT: Roberts, Christopher J.
;   APPLICANT: Van 't Veer, Laura Johanna
;   APPLICANT: Van de Vijver, Marc J.
;   APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 912
;   LENGTH: 1679
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-912

Query Match   50.8%;   Score 952.8; DB 7; Length 1679;
Best Local Similarity   80.2%;   Pred. No. 2.8e-206;
  Matches 1210; Conservative   0; Mismatches 252; Indels   46; Gaps   6;

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Db  1406 AACTGAACATTCCAGAGCCGTGTAGTGAATCACGTAAAGCTAAAATGATCCCCAGCTGTT 1465
         ||||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||||

Qy  1544 GCTGCATA 1551
         ||||||||
Db  1466 TATGCATA 1473
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Search completed: January 11, 2006, 00:21:54
Job time : 1646 secs

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Qy   404 CTGGGCAGTTGATGCCATGGCTGACTGGTACTTTGGGAATTTTTGTGTAAGGCTGTCCA 463
         |||||||||||||||||  |||| || ||||||||||||||| ||  |||||||| ||||
Db   367 CTGGGCAGTTGATGCCGTGCGAAACTGGTACTTTGGGAACTTCCTATGCAAGGCAGTCCA 426

Qy   464 TATCATCTACACTGTCAACCTCTACAGACGCGGTCCTCATCCTGGCCTTCATCAGCCTGGA 523
         | |||||||||| |||||||||||||| | ||| ||||||||||||||||||||||| |||
Db   427 TGTCATCTACACAGTCAACCTCAACCTCTACAGCAGTGTCCTCATCCTGGCCTTCATCTCTGA 486

Qy   524 CCGGTACCTCGCCATTGTCACGGCCACCAACAGTCAAGAGGCCAAGAGAAACTGCTGGCTGA 583
         |||||||||||||| |||||||||||||||||||||| ||||||| ||||||||||||||||
Db   487 CCGCTACCTGGCCATCGTCACGGCCACCAACAGTCAGAGGCCAACAGTCAGAGGAAGCGTGTTGGCTGA 546

Qy   584 AAAGGCAGTCTATGTGGGGCGTCTGACTCCAGCCCTCCTCCTGACTATACCTGACTTCAT 643
         |||| ||||| |||||||||||||| |||||| ||||||||||| ||| ||| |||||||
Db   547 AAAGGTGTCTATGTTGGCGTCTGATCCCGCCCTCCTGCTGACTATTCCCGACTTCAT 606

Qy   644 CTTTGCCGACGTCAGCAGGGGACATCAGTCAGGGGGATGACAGGTACATCTGTGACCG 703
         |||||||||||||                           TCAGTGAGGCAGATGAGCATATATCTGTGACCG
Db   607 CTTTGCCAACG---------------------TCAGTGAGGCAGATGAGCATATATCTGTGACCG 651

Qy   704 CCTTTACCCGGATAGCCTGTGGATGGTGGTGTTTCAATTGTGTTCCAGCATAATGGTGGTCT 763
         ||||||||||    | |||||||||||||||||||| |||||||||||||||| |||||| |
Db   652 CTTCTACCCCAATGACTTGTGGGTGTTGGTGTGTTTCCAGTTTTCAGCACCATCATGGTTGGCCT 711

Qy   764 CATCCTGCCCGGCCGGATCGTCATCGTCTCCTGTTACTGCATCATCATCTCTCAAGCTGTCACA 823
         ||| || |||||   || |||||||||| |||| |||| |||| ||||||||||||||| ||||
Db   712 TATCCTGCCTGGTATTGTGTCATCGTCTCCTGCTATTGCATTATCATCTCTCCAAGCTGTCACA 771

Qy   824 CTCCAAGGGCCACCAGAAGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTCAGCTTT 883
         |||||||||||||||||| ||||||||||| ||||| ||||||||||||||||| |||||
Db   772 CTCCAAGGGCCACCAGAAGCGCAAGGCGCAAGGCCCTCAAGACCAGTCATCCTCATCCTGGCTTT 831

Qy   884 CTTTGCTGCTCGGCTGCCATATATGTGGGGATCAGCAGCATTGGGG 943
         | |||||||||||| ||||||||||| |||||||||| ||||||| ||||||||||| ||
Db   832 CTTCGCCTGTGTTGGCTGCTGCTGGCCTGCTCTACTACATTGGGATCAGCAGCATCAGCATCCTGGA 891

Qy   944 AGTCATCAAGCAAGGATGTGACTTCGAGAGCATTGTGACAAGTGATCTTCCATCACAGA 1003
         | |||||||||||||| ||||| |||||| |||||| |||||||||  |||||||||| |
Db   892 AATCATCAAGCAAGGGTGTGAGTTTGAGAACACTGTGCAACAAGTGGATTTCCATCACCGA 951

Qy  1004 GGCCCTCGCCTTCTTCCACTGTGCCTGCAACCCCATCCTCCTATGCCTTCCTCGGGGCCAA 1063
         |||||||||||| || |||| || ||||||| |||||||| ||||| |||| ||||||||
Db   952 GGCCCTAGCTTCTTCTTCCACTGTTGTCTGCAACCCCATCCTCTATGCTTTGTTCCTTGGAGCCCAA 1011

Qy  1064 GTTCAAAAGCTCGTCGCCAGCATGCAATGCACTCAACTCAATGAGCAGCAGAGGCTCCAGCCTCCAAGAT 1123
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Qy  1124 CCTTTCCAAAGGAAGACGGGGTGGACACTCTTCCGTCTCCACTGTTTCCACTGACTGTTCCAG 1183
         ||| ||||||||||||| ||||||||||| |||| || ||| |||| |||||| |||| ||||
Db  1072 CCTCTCCAAAGGAAGACGGGAGGTGGACATTCATCATCTGTTTCCACTGACTGTTCAAG 1131

Qy  1184 TTTTCACTCCAGTCAACCCTTATGCAAAGACTTATATATGCAAAGACTTTT--------TTTTATACGATAAATAA 1243
         |||||||||||| |||||  |||| |||| ||| ||| ||||| ||||||        ||||| || ||| |||
Db  1132 TTTTCACTCCAGTCAACGCTGTCAACACAGATGTAAAAGACTTTT-----------TTTATACGATAAATA 1183

Qy  1244 GAACTTTTTATGTTACACATTTCCAGATATAGAAGACTGACCAGTCTTGTACAGTTTT 1303
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Qy  1304 GAACTTTTTTTTATTGACTGTTGGGAGTTTAATGTTCCTTTTGTTTTTGTGAAGGTTGACT 1363
         || ||| ||||||| ||| |||||  ||| |||||| ||| ||||| |||||||||
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Qy  1364 TAATTATATAAATATTGTTTTTTTGTTTTTTCATGTGAATGAGCGTCTAGGCAGGACCT 1423
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Qy  1424 GTGGCCAAGTTCTTAGTAGCTGTTTATCTGTGTGTAGGACTGTGAACTGTGAGAGGAAGA 1483
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Qy  1484 AACTGAACATTCCAGAATGTGTGGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTT 1543
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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:    January 10, 2006, 20:47:07 ; Search time 338 Seconds
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Title:          US-09-367-052-1
Perfect score:  1877
Sequence:       1 ccatcctaatacgactcact.........aaaaaaaaaaaaaaaa 1877

Scoring table:  IDENTITY NUC
                Gapop 10.0, Gapext 1.0

Searched:       4637633 seqs, 36453275 residues

Total number of hits satisfying chosen parameters:     9275266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications NA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1169.6	62.3	1651	7	US-11-136-527-2630	Sequence 2630, Ap
2	1074.4	57.2	1643	7	US-11-136-527-108	Sequence 108, App
3	960.4	51.2	1662	7	US-11-028-922A-3	Sequence 3, Appli
4	.950	50.6	1400	7	US-11-136-527-6726	Sequence 6726, Ap
5	932.4	49.7	8747	6	US-10-955-054A-141	Sequence 141, Appl
6	905.6	48.2	1050	7	US-11-028-922A-4	Sequence 4, Appli
7	890.4	47.4	1400	7	US-11-136-527-4204	Sequence 4204, Ap
8	859	45.8	1225	6	US-10-955-054A-112	Sequence 112, Appl
9	808	43.0	1102	7	US-11-136-527-121	Sequence 121, Appl
10	198.4	10.6	246960	7	US-11-121-086-8	Sequence 8, Appli
11	176.4	9.4	1680	7	US-11-136-527-153	Sequence 153, App
12	175	9.3	1324	7	US-11-136-527-2373	Sequence 2373, Ap
c 13	170	9.1	1433	6	US-10-750-185-54253	Sequence 54253, A
c 14	170	9.1	1433	6	US-10-750-623-54253	Sequence 54253, A
15	168.6	8.9	1400	7	US-11-136-527-4249	Sequence 4249, Ap
16	167.2	8.9	3062	6	US-10-995-561-120	Sequence 120, App
17	167.2	8.9	3100	6	US-10-775-169-254	Sequence 254, App
18	167.2	8.9	3101	6	US-10-995-561-119	Sequence 119, App
19	167.2	8.9	30151	6	US-10-995-561-13239	Sequence 13239, A
20	165.2	8.8	1348	7	US-11-136-527-3311	Sequence 3311, Ap
21	160.4	8.5	3177	7	US-11-127-877-25	Sequence 25, Appl
22	153	8.2	1960	7	US-11-136-527-617	Sequence 617, Appl
23	146.6	7.8	1059	7	US-11-068-686-19	Sequence 19, Appl
24	145.2	7.7	3383	7	US-11-068-686-1	Sequence 1, Appl
25	145.2	7.7	3655	7	US-11-127-877-24	Sequence 24, Appl
26	142.4	7.6	3655	6	US-10-995-561-6	Sequence 6, Appl
27	142.4	7.6	18059	6	US-10-995-561-13195	Sequence 13195, A
28	142.2	7.6	1383	7	US-11-136-527-3271	Sequence 3271, Ap
29	138.8	7.4	653	6	US-10-750-185-39564	Sequence 39564, A
30	138.8	7.4	653	6	US-10-750-623-39564	Sequence 39564, A
31	136.4	7.3	2273	7	US-11-127-877-23	Sequence 23, Appl
32	136	7.2	1457	7	US-11-136-527-3492	Sequence 3492, Ap
33	136	7.2	1689	7	US-11-136-527-3281	Sequence 3281, Ap
34	126	6.7	1365	7	US-11-136-527-2610	Sequence 2610, A
c 35	125	6.7	706	6	US-10-750-185-32790	Sequence 32790, A
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37	121.2	6.5	1339	7	US-11-136-527-4061	Sequence 4061, Ap
38	121.2	6.5	2580	7	US-11-136-527-3525	Sequence 3525, Ap
39	119.6	6.4	2156	7	US-11-136-527-3843	Sequence 3843, Ap
40	118	6.3	1450	7	US-11-136-527-3841	Sequence 3841, Ap
41	118	6.3	3219	7	US-11-136-527-4059	Sequence 4059, Ap
42	118	6.3	3295	7	US-11-136-527-3736	Sequence 3736, Ap
43	113.2	6.0	1915	7	US-11-068-686-3	Sequence 3, Appl
44	113.2	6.0	1945	7	US-11-127-877-27	Sequence 27, Appl
45	110.8	5.9	1251	7	US-11-122-849-1	Sequence 1, Appl

ALIGNMENTS

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RESULT 1
US-11-136-527-2630
; Sequence 2630, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2630
; LENGTH: 1651
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2630

Query Match             62.3%;  Score 1169.6;  DB 7;  Length 1651;
Best Local Similarity   84.2%;  Pred. No. 2e-215;
Matches 1470;  Mismatches 148;  Conservative 4;  Indels 124;  Gaps 9;

Qy    136 TGAGTATATACACTTCTGATAACTACTCTGAGGAAGTGGGGTCTGGAGACTATGACTCCA 195
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Db      2 TGGAAATATACACTTCGGATAACTACTCCGAAGAAGTGGGGTCTGGAGACTATGACTCCA 61

Qy    196 ACAAGGAACCCTGCTTCCGGATGAGAAACGTCCATTTCAATAGGATCTTCCTGCCCACCA 255
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Db     62 ACAAGGAACCCTGCTTCCGGATGAGAAAACGAAAACTTCAACAGGATCTTCCTGCCCACCA 121

Qy    256 TCTACTTCATCATCTTCTTGACTCGGCATAGTCGGCAATGATTGGGTGATCCTGGTCATGG 315
          |||| | | ||||||||||||||||||||||||||||||||  |||| || |||||||||
Db    122 TCTATTTTATCATCTTCTTGACTCGGCATAGTCGGCAATGGGGTTGGTAATCCTGGTCATGG 181

Qy    316 GTTACCAGAGAAGTAAGGAGCATGACGGACAAGAAGTACCGGCTGCACCTGTCAGTGGCTG 375
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Db    182 GTTACCAGAGAAGCTGAGGAGCATGACAGACAGACAAGAGCCGGCTGCACCTGTCCGTGGCTG 241

Qy    376 ACCTCCTTTGTCATCACACTCCCCTTCTCGGCAGTTGATGCCATGGTCAGTGACTGGTACT 435
          |||||||||||||||||||||||||||||||| ||| |   ||||| ||| |||||||||
Db    242 ACCTCCTTTGTCATCACACTCCCCTTCTCGGCCAGTGACGGACGGCCATGGCCATGACTGGTACT 301

Qy    436 TTGGGAAATTTTTGTGTAAGGCTGTCCATATCATCTCAACCTGTCAACCTCTACAGAGCG 495
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Db  1367  GAACGCTCCAGAATGTGTCGTAAATCGGATAAAGCTAGAAGTGACCCT-AGCTGTCGCTG  1425
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Qy  1548  CATAATCTCTCATTCCGAGGAGCACCCCACCCCACCCCATTCTTAA  1607

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Qy  1608  ATTGTTTGGTTATGCTGTGTGATGGTTGTTTGTTTGGTTGTTTGTTGTTGTTGTTT  1667

Db  1460  --------ATTGTTTGGTTGTTGCGTGTG  1480

Qy  1668  TTTTTTCTGTAAAAGATGGCACTTAAAACCAAAGCCTGAAAATGGGTAGAAATGCTGGG  1727

Db  1481  GTTTCTCTGTAGAGAGATGGCACTTAAAACCAAAGCCTGAAATGGT-ATAGAAATGCTGG-  1538

Qy  1728  GTTTTTTTGTTTGTTGTTTTTCAGTTTCAGAGTAGAATTGACTTCCAGTCCCTACAA  1787

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Qy  1848  AAAAAA  1853

Db  1646  AAAAAA  1651
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Best Local Similarity   80.4%;   Pred. No. 3.6e-197;
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Qy  199  AGGAACCCTGCTTCCGGGATGAAAACGTCCATTTCAATAGGATCTTCCTGCCCACCATCT  258

Db  108  AGGAACCCTGCTTCCGGGATGAAAAACGAAAACTTCAACAGGATCTTCCTGCCCACCATCT  167

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Db  168  ATTTTATCATCTTCTTGACTGACATAGTGGCATAGTGGGTAATCCTGGTCATGGGTT  227

Qy  319  ACCAGAAGAGAGCTAAGGAGCTAAGGAGGAGCACGAGCAAGTACCGGCTGCACCTGTCCGTCAGTGGCTGACC  378

Db  228  ACCAGAAGAGCTGAGGAGCATGACAGACAAGTACCGGCTGCACCTGTCCGTGGGCTGACC  287

Qy  379  TCCTCTTTGTCATCACACTCCCCTTCTCGGGCAGTTGATGCCATGGCCATGGACTGGTACTTTG  438
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Db  362  TTCTCATCCTGGGCCTTCATCAGCTGGACCGGTACCTCGCCATTGTCCACGCCACCAACA  421

Qy  556  GTCAAAGGCCAAGGAAACTGCTGGCTGCTGAAAAGGCCGTCTATGTGGGCGTCTGATCCCAG  615

Db  422  GCCAGAGCGGAGGAAGCTGCTGCTGAAAAGGCCGTCTATGTGGGCGTCTGATCCCCG  481

Qy  616  CCCTCCTCCTGACTATACCTGACTTCATCTTGCCGACGTCAGCCAGGGGACATCAGTC  675

Db  482  CCCTCCTCCTGACATCATCTTCGCCGATGTCAGCCAGGGGAC--------  534

Qy  676  AGGGGGATGACAGTACATCGTGACCGCCTTACCCCGATAGCCTGTGTGGATGGTGGTGT  735

Db  535  -------GGCAGTACATCGTGACCGCCTTTACCCCGACAGCCTGTGTGGATGGTGGTGT  586

Qy  736  TTCAATTCCAGCATATAATGGTGGGTCTCATCGTCATCCTCTCCTGTT  795

Db  587  TCCAGTTCCAGCACATCATGGTGGGTCTCATCGTCATCCTGTCCTGTT  646

Qy  796  ACTGCATCATCATCTCTAAGCTGTCACACTCCAGAATGTGCCTGCGCAAGGCGCCCTCA  855

Db  647  ACTGCATCATCATCTCCAAGCTGTCACACTCCCAAGAATGTGCCTGCGCAAGGCGCCCTCA  706

Qy  856  AGACAGCAGTCATCCTCATCTAGCTTTTCTTTGCCTGGCTGCGTCGCCATATTATGTGGGGA  915

Db  707  AGACTACGGTCATCTCATCCTGCCTTTCTTGCCTGCTGCGTACCGTATTACGTGGGGA  766

Qy  916  TCAGCATCGACTCCTTCATCCTTTTGGAGTCATCAAGCAAGGATGTGACTTCGAGAGCA  975

Db  767  TCAGCATCGATCCTTCATCCTTTTGGAGTCATCAAGCAAGGATGTGAGTTCGAGAGCG  826

Qy  976  TTGTGCAAGTGGATCTCCATCACAGAGGCCCTGCCTTCTTCCACTGTTGCCTGAACC  1035

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Qy  1036  CCATCCTCTATGCCTTCCTCGGGGCCAAGTTCAAAAGTCTGCCCAGCATGCACTCAACT  1095

Db  887  CCATCCCTACGCCTTCCTCGGGGCCAAATTCAAGAGCTCCGCGCAGCAGCACTCAATT  946

Qy  1096  CCATGAGCAGAGGCTCCAGCCTCAAGATCCTTTCCAAAGGAAAGCGGGGTGGACACTCTT  1155

Db  947  CCATGAGCAGAGGCTCCAGCCTCAAGATCCTTTCCAAAGGGAAACGGGGTGGACACTCTT  1006

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Qy  1326  GGGAGTTTATGTTCCTCT------AGTTTTTGTGAGGTTTGACTTAATTAATTTATATAAATA  1378

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Qy  1379  T---------TGTTTTTTGTTTGTTGTTTTCATGTGAATGAGCGTCTAGGCAGGACCTGTGG  1427

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Qy  1428  CCAAGTTCTTAGTAGCTGTTTATCTGTGTGTTTAGGACTGTAGAACTGTGAGGGAGAAACT  1487

Db  1307  CCAAGTTCTTAGTCGTTAGTGTGTCTGTGTGTAGGACTGTGTAGAGGAGGAACT  1366

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Db 288 ||||||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||
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Qy 498 GGAAATTTTTATGTGAAGGCTGTGCATATCATCTACACCGTCAACCTTTACAGCAGTGTTT

Db 342 GGAAATTTTTATGTGAAGGCTGTGCATATCATCTACACCGTCAACCTTTACAGCAGTGTTT
Qy 401

Db 499 TCATCCTGGCCTTCATCAGCCTGGACCGGTACTTCGCCATTGTCCAGGCCACCAACAGTC
Qy 558 TCATCCTGGCCTTCATCAGCCTGGACCGGTACTTCGCCATTGTCCAGGCCACCAACAGCC

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Qy 461

Db 559 AAAGGCCAAGGAAACTGCTGCTGGCCAGTCTATGTGGGCGTCTGAAAGCC----------
Qy 618   AGAGGCGCAGGAAGCGCTGCTGGCTGGCTGCTGGCTGGAAAAGCC

Db 462 AGAGGCGCAGGAAGCGCTGCTGGCTGGCTGCTGGAAAAGCC
Qy 493

Db 619 TCCTCCTGACTATACCTGACTTCATCTTTGCCGACGTCAGCCAGCCAGGGGACATCAGTCAGG
Qy 678

Db 494 ------------------GCATCATCTTCGCCGATGTCAGCCAGGGGGAC--------
Qy 526

Db 679 GGGATGACGAGTACATCTGTGACCGCCTTACCCTGAGTAGCCTGGATGGTGCGTGTTTC
Qy 738   GGCAGGTACATCTGTGACCGCCTTTACCCTGAGTAGCCTGGATGGTGCGTGTTCC

Db 527 ------GGCAGGTACATCTGTGACCGCCTTTACCCTGAGTAGCCTGGATGGTGCGTGTTCC
Qy 581

Db 739 AATTCCAGCATATAATGGGGTCTCATCGCTGCCCGGCATCGTCATCCTCTGTTACT
Qy 798   AGTTCCAGCACATCATGGGGTCTCATCGCTGCCCGGCATCGTCATCCTGTCCTGTTACT

Db 582 AGTTCCAGCACATCATGGGGTCTCATCGCTGCCCGGCATCGTCATCCTGTCCTGTTACT
Qy 641

Db 799 GCATCATCATCTCTAAGCTGTCACACTCCAGAGACGCGCAAGGCCCTCAAGA
Qy 858   GCATCATCATCTCCAAGCTGTCACACTCCAAGAGCGCAAGGCCCCTCAAGA

Db 702 CTACGGTCATCATCCTCCTTCGGCTTTCTTCGCTGCTCGGCTACCGTATTACGTGGGGATCA
Qy 761

Db 919 GCATCGACTTCCTTCATCCTTTGGAGTCATCAAGCAAGGATGTGACTTCGAGAGCATTG
Qy 978   GCATCGACTTCCTTCATCCTTTGGAGGTCATCAAGCAAGGATGTGAGTTCGAGAGCGTCG

Db 762 GCATCGACTTCCTTCATCCTTTGGAGGTCATCAAGCAAGGATGTGAGTTCGAGAGCGTCG
Qy 821

Db 979 TGCACAAGTGGATCTGGATCTCCATCACAGAGGCCCTGCCCTTCAAAAGTCTGCCCAGCACTCAACTCCA
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Qy 881

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Qy 1061

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Qy 1269   ATMATATATATATATATATATATATATGMCAAAGAACTTTTTTTATGTTACACATTTCCC

Db 1062 ATMATATATATATATATATATATATATGMCAAAGAACTTTTTTTATGTTACACATTTCCC
Qy 1121

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Qy 1329   AGATATAAAGAGACTGACCAATCTTGTACAGTTTTTTTTTATTGACTGTGGGA

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Qy 1181

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Qy 1382   TGACTCCATGGAAGGAACCCGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCT

Db 1182 TCTCTAGTTWTTGTGTCTGTTTCACGTGTGTRAGGTTGAYTTAATTTATATAAATAAATATTCG
Qy 1241

Db 1383 TTT--------TTGTTTGTTCATGTGATGAATGAGCGTCTAGGCAGTCGTCAGCAGAACGTGTGGCCAA
Qy 1431   KTTTTTCYGKTGKTKGTCTGTTTCACGTGAGTGTCTAGGCAGACCTGTGGCCAA

Db 1242 KTTTTTTCYGKTGKTKGTCTGTTTCACGTGAGTGTCTAGGCAGACCTGTGGCCAA
Qy 1301

Db 1432 GTTCTTAGTAGTCTGTGTGTGTGTAGGACTGTGAGGAAGAAAACTGAAC
Qy 1491   GGTCATGGGTTACCAGCAAGGATGTAGAGGAAGAAACTGAAC

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Qy 1361

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Qy 1551

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Qy 1611

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Qy 1535

Db 1732 TTTTTGTTTGTTTGTTTTTCAGTTTTCAAGGTAGATTGACTTCCTACCTACAAATGT 1791
Qy 1791

Db 1536 TTY----------TTTCAGTTTCAAGGTGATTTGATTTTCAGTACCTACACAATGT 1581
Qy 1581

Db 1792 ACAGTCTTGTATTACATTGTTAATAAAGTCAATGATAAACTTAAAAAAAAAAAAA 1851
Qy 1851

Db 1582 ACAGTCTTGTTGTATTATGTTGTTAATAAAGTCAATGTAAACTTRMAAAAAAAAAAAAAA 1641
Qy 1641

Qy 1852 AA 1853
      ||
Db 1642 AA 1643

RESULT 3
US-11-028-922A-3
; Sequence 3, Application US/11028922A
; Publication No. US2005271639A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCF-7019
; CURRENT APPLICATION NUMBER: US/11/028,922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-028-922A-3

Query Match   51.2%;   Score 960.4; DB 7; Length 1662;
Best Local Similarity   76.3%;   Pred. No. 2.7e-175;
Matches 1371; Conservative   0; Mismatches 291; Indels 136; Gaps 10;

Qy 68 CTGAGGCGTTGGTGTCTCCGTAACCACCACGGCTAACGGCTGTTGCCATGGAACC 127
        |||||||||| ||||| ||||| ||||||||||||||||||| ||||||||||
Db 1   CCGAGGGCCTGAGTGCTCCAGTAGCCACCGCCATCTCGAGAACCAGCCAGGTTACCCATGA-- 58

Qy 128 GATCAGTGTGAGTATATACACTTCTGATAACTACTCACACACGAGAAGTGGGGTCTGGAGGGACTA 187
        |||| ||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db 59 ---GGGGATCAGTAGTATTATCAGATAACTACTCACACACGAGGAAATGGGCTCAGGGGACTA 115

Qy 188 TGACTCCAACAAGAACCTGCTTCCGCGGCTTCCGGATGAAAACGTCCATTTCAATAGGATCTTCCT 247
        |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 116 TGACTCCATGGAAGGAACCCGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCT 175

Qy 248 GCCCACCATCTACTTCATCATCTTCATCTTAACTGGGCAAGTACCGGCTGCACCTGATCCT 307
        |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db 176 GCCCACCATCTACTTCATCATCTTCATCATCTTAACTGGGCATGTGGGCAAGTACCGGCACCTGTC 235

Qy 308 GGTCATGGGTTACCAGCAAGGATGTAGAGGAAGAAACTGAAC 367
        ||||||||||||||||||||||||||||||||||||||||||
Db 236 GGTCATGGGTTACCAGCAAGGACGACAAGTACGCAGGGGTGCACCTGTC 295

Qy   368 AGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGGGCAGTTGATGGCCATGGCTGA 427
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   296 AGTGGCCGACCTCCTCTTTGTCATCACACGGCTTCCCCTTCTGGGCAGTTGATGGCCGTTGGCCAAA 355

Qy   428 CTGGTACTTTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTTACACTGTCAACCTCTA 487
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   356 CTGTTACTTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCACACAGTCAACCTCTA 415

Qy   488 CAGCAGCGTTCTCATCCTGCCTCTGGCCTCATCAGCCTGACCGTACCTCGCCACGC 547
         ||||||||||||||||||||||||||||||||||||||||||||
Db   416 CAGCAGTGTCCTCATCCTGCCTCATCGGCCTCATCGGACCGCTACCTGGCCATCGTCCCAGC 475

Qy   548 CACCAAACAGTCAAGGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTGGGCGTCTG 607
         ||||||||||||||||||||||||||||||||||||||||||||
Db   476 CACCAACAGTCAGAGGGCCAAGGAGAGCCGTGTGTGGCTGAAAAAGGGTGGTCTATGTTGGCGTCTG 535

Qy   608 GATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTTGCCGACGTCAGCCAGGGGGA 667
         ||||||||||||||||||||||||||||||||||
Db   536 GATCCCTGCCCTCCTGCTGACTATTCCCGACTTCATCTTTTGCCAACG----------- 582

Qy   668 CATCAGTCAGGGGATGACAGGTACATCTGTGACCGCGCCCTTACCCGATAGCCTGTGAT 727
         ||||||| ||||||||||||||||||||||||| |||||||
Db   583 --TCAGTGAGGCAGATGACAGAGATATCTGTGACCGCGTCTGCTGCTGCTTCAGCTCTGTGAGTT 640

Qy   728 GGTGGTGTTCAATTCAGCATATAATGGTGGTCTCATCCTGCCCGGCATCGTCATCCT 787
         |||||||||||||||||||||| |||| | |||||||||
Db   641 GGTGTGTGTTCAGCAGTTCAGCTCGCCTTATCCTGCCTGGTATTGTCATCCT 700

Qy   788 CTCCTGTGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAAGGGCCACCCAGAAGCGCAA 847
         |||| |||| ||||| ||||| |||||||| |||||||||||||| |||||||||||
Db   701 GTCCTGCTATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAGCCGCAA 760

Qy   848 GGGCCCTCAAGACGACAGCAGTCATCCTCATCCTCTAGCTTCTTGCTTGCTGCTGCCTGCCTGCCTTACTA 907
         |||||||||||||||||||||||||||||||||||||||| |||||||| |||||||||
Db   761 GGGCCCTCAAGACCACCAGTCATCCTCATCCTCTGGGCTTCTTCGCCTGTTGGCTGCCTTACTA 820

Qy   908 TGTGGGGATCAGCATGCATCGACTCCTTTGGGAGTCATCAAGCAAGGATGGACTT 967
         |||||| |||||||||||||||||||||||| |||| |||||||||||| |||||
Db   821 CATTGGGGATCAGCATCAGCATCGACTCCTTTCATCATCCTGAAATCATCAAGCAAGGTGAGTT 880

Qy   968 CGAGAGCAATTGTGCACAAGTGGATCTCCATCACAGAGGCCCTGCCTTCTTCCACTGTTG 1027
         |||||||| ||||||||||||||||||||||||||||||||||||| ||||||
Db   881 TGAGAAACACTGTGCACAAGTGGATTTCCATCACCAGGGCCCTAGCTTTCTTCCACTGTTG 940

Qy 1028 CCTGAACCCATCCTATGCCTTCCTGCGGGGCCAAGTCAAAAGCTCTGCCCAGCATGC 1087
         |||||||||||||||||||||||||||||||||||| ||||||||||
Db   941 TCTGAACCCCATCCTATGCTTTCCTGTTGAGCCAAATTAAAAACCTCTGCCCAGCACGC 1000

Qy 1088 ACTCAACTCCATCATGAGCAGAGCCTCAAGATCCTTCAAAGGAAAGCGGGGTGG 1147
         |||| |||||||||||||||||||||||| |||||||||||||||||
Db 1001 ACTCACCTGGTGAGCAGAGAGGGTCCAGCCTCAGATCCTTCCCAAAGGAAAGCGAGGTGG 1060

Qy 1148 ACACTCTTCCGTCTCCCACGGAGTCAGAATCCTCAGTTTTCACTCCAGCTAA----- 1207
         |||| |||||| ||||||| |||||||||||||||| ||||||||||
Db 1061 ACATTCATCGTGTTTCCACTGAGTCTTCAAGTTTCAAGTTTTCACTGAGTCTTCAAGTTTCAA 1112

Qy 1208 CAAAGACTTATATATATAATATATATATGATAAAGAACTTTTTTTATGTTACACATTTT 1267
         |||| ||||||||||| ||| ||||||||||||||||||||||
Db 1113 CACAGATGTAAAAGACTTTTTTTTATACGATAAATAACTTTTTTTTAAGTTACACATTTT 1172

Qy 1268 CCAGATATAAGAGACTGACCAGCCTCGTGTACAGTTTTTTTTTTTAATTGACTGTGTGG 1327
         ||||||||||||||||||||||| ||||||| ||||||||||||||
Db 1173 TCAGATATAAAGAGACTGACCAATATTGTACAGTTTGTACAGTTTTTTATTGCTTGTTGGATTTTTGT-- 1229

Qy 1328 GAGTTTATGTTCCCTCAGTTTTGTGAGGTTTGACTTAATTTATAAATATTGTTTTT 1387
         |||||||| ||||| ||||| |||||||| |||||||||
Db 1230 ---CTTGTGTTTCTTTAGTTTTGTGAAGTTTAATTGACTTATTTATA---TAAATTTT 1282

Qy 1388 GTTTGTTCATGTGAATGAGCGGTCTAGGCAGGACCTGTCGGCCAAGTTCTTAGTAGTGTT 1447
         |||||||| ||||||||||||||||||||||| ||||||||||||||||||
Db 1283 TTTTGTTTCATATTGATGTGTGTCTAGGCAGGACCTGGCCAAGTTCTTAGTTGCTGTA 1342

Qy 1448 TATCTGTGTGTAGGACTGTAGAACTGTAGAGGAGAAAACTGAACATTCCAGAATGTGTGG 1507

Db 1343 TGTCTCGTGTGGTAGGACTGTGAGAA------------AAGGGACTGAACATTCCAGAGCGTGTAG 1394
         |||||||| |||||||||||||||||||

Qy 1508 TAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGGTGCTGCATATCTTCATTCCGAG 1567
         ||||||||| |||||||||||||
Db 1395 TGAATCACGTAAAGCTAGAAATGATCCCCAGCTGTTTATGCATAGATAATCTCTCCA--- 1451

Qy 1568 GAGCACCCCACCCCCACCCCCACCCCCATTCTAAATTGTTGGTTATCGTCGTGT 1627
         ||||||||
Db 1452 GAGCAC--- 1451

Qy 1628 GATGGTTTGTTTGGTTTTTTGTTGTGTTGTTTTTTTTTCTGTAAAAGATGGC 1687
         ||| |||||||||||||||||||||||||||||||||||||||
Db 1452 -----TTCCCGTGGAACGTTTTCCTGTGTTCTTAAGACGTGATTTTGCTGTGAGAAGATGGC 1506

Qy 1688 ACTTAAAACCAAAGCTGAAATGGTGGTAGAAATGCTGGGGTTTTTTGTTGTTGTT 1747
         ||||||||||||| |||||||||||||||||||||||||||||| |
Db 1507 ACTTATAACCAAAGCCCAAAGTGGT-ATAGAAATGCTGG----------------T 1545

Qy 1748 TTTTCAGTTTTCAAGAGTAGATTGACTTCAGTCCTACAAATGTACAGTCTTGTATTACA 1807
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1546 TTTTCAGTTTTCAGGAGTGGGTTGATTTCAGCACTAC-AGTGTACAGTCTTGTTATTAAG 1604

Qy 1808 TTGTTAATAAAAGTCAATGATAATCTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1865
         |||||||||||| |||| ||||||| ||||||||||||||||||||||||||||||
Db 1605 TTGTTAATAAAAGTACATGTTAAACTTAAAACTTAAAAAAAAAAAAAAAAAAAAAAAAAA 1662

RESULT 4
US-11-136-527-6726
; Sequence 6726, Application US/1113527
; Publication No. US2005028757OA1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6726
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6726

Query Match   50.6%;   Score 950;   DB 7;   Length 1400;
Best Local Similarity   82.8%;   Pred. No. 2.5e-173;
Matches 1239;   Mismatches   4;   Conservative   9;   Indels   124;   Gaps   9;

Qy   386 TGTCATCACACTCCCCTTCTGGCCAGTTGATGGCCATGGCTGACTGCTGACTTGGGAAATT 445
         |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   1 TGTCATCACACTCCCCTTCTGGGCAGTTGATGGCCATGGCTGACTGCTGACTTGGGAAATT 60

Qy   446 TTTGTGTAAGGCTGTCCATATCATCTTACACTGTCAACCTCTACAGCAGCGTTCTCATCCT 505
         ||||||||||||| |||||||||||||||||| ||||||||||||||| ||||||||||
Db   61 TTTATGTAAGGCTGCATCATCATCTTACACCGTCAACCTTTACAGCAGTGTTCTCATCCT 120

Qy   506 GGCCTTCATCAGCCTGGACCGGTACCTCGCCATTGTCACGCCACCAACAGTCAAAGGCC 565
         |||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   121 GGCCTTCATCAGCCTGGACCGGTACCTTGCCATTGTCACGCCACCAACAGCCCAGAGCGC 180

Qy   566 AAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTGGGCGGTCGTCGGTCCTCCT 625
         ||||||| ||||||||||||||||||||||||||| ||||||||||||||
Db   181 GAGGAAGCTGCTGGCTGAAAAAGGCAGTCTATGTGGGTGTCGTCGGATCCCTCCT 240

Qy   626 GACTATACCTGACTTCATCTTTGCCGACGTCAGCCAGGGGACATCAGTCAGCAGCAGGGGATGA 685
         |||||||||||||||||||||| ||||||||||||||||||||||| |
Db   241 GACTATCCCTGACTTCATCTTTTGCCGACGTCAGCCAGGGGGAC-----------GG 285

Db   1288   ---GTTTTTCTTTCAGTTTCAGTTTCAAGGGTGGATTGATTTCAGTAGTACCTACAAATGTACAGTC   1344

Qy   1798   TTGTATTACATTGTTAATAAAGTCAATGATAAACTTAAAAAAAAAAAAAAA   1853

Db   1345   TTGTATTATGTTGTTAATAAAGTCAATGATAAACTTGCAAAAAAAAAAAAAAA   1400

RESULT 5
US-10-955-054A-141
; Sequence 141, Application US/10955054A
; Publication No. US2005266420A1
; GENERAL INFORMATION:
;   APPLICANT: PUSZTAI, LAJOS
;   APPLICANT: SYMMANS, W. FRASER
;   APPLICANT: HESS, KENNETH R.
;   APPLICANT: AYERS, MARK
;   APPLICANT: STEC, JAMES
;   TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
;   FILE REFERENCE: UTXC:880US
;   CURRENT APPLICATION NUMBER: US/10/955,054A
;   CURRENT FILING DATE: 2004-09-30
;   NUMBER OF SEQ ID NOS: 195
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
;   LENGTH: 8747
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-955-054A-141

Query Match   49.7%;   Score 932.4;   DB 6;   Length 8747;
Best Local Similarity   81.5%;   Pred. No. 1e-169;
Matches 1156;   Conservative   0;   Mismatches 221;   Indels   41;   Gaps   5;

Qy   134   TGTGAGTATATACACTTCTGATAACTACTCTGAAGAAGTGGGGTCTGGAGACTATGACTC   193

Db   4861   TTTGCAGATATACACTTCAGATAACTACACCGAGGAAATGGGCTCAGGGGACTATGACTC   4920

Qy   194   CAACAAGGAACCCTGTTCCCGGATGAAACGTCCATTTCAATAGGATCTTCCTGCCCAC   253

Db   4921   CATGAAGGAACCCTGTTCCCGTTCCCGTTCCGTGAAGAAAATGCTAATTCAATAAAATCTTCCTGCCCAC   4980

Qy   254   CATCTACTTCATCATCTTCTTAACTGGCATAGTGCATAGTGGCAATGATTGGTCATCCTGTCAT   313

Db   4981   CATCTACTTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATTCCTGTCAT   5040

Qy   314   GGGTTACCAGAAGAGCTAGGAGCTAAGAGACGTAGGAGCATGACGACGGAAGTACCGGCTGCAGTGGC   373

Db   5041   GGGTTACCAGAAGAAACTGAGAGAACGTGACATGAGAAGCATGAGAAGCATGACGACGGACAAGTACCGGCTGCAGTGGC   5100

Qy   374   TGACCTCCTTGTCATCACATGCTGCCTGAAAGGCAGTGTTGATGCCATGGGACTGGTA   433

Db   5101   CGACCTCCCTCTTGTCATCACACGCTTCATCCTTCTCGGGCAGTGTGATGCCGTGGCAAACTGGTA   5160

Qy   434   CTTTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTACACTGTCAACCTCTACAGCAG   493

Db   5161   CTTTGGGAACTTCCATGCAAGGCAGTCCATTGTCCATTGTCACAGTCAACCCTCTACAGCAG   5220

Qy   494   CGTTCTCATCCTGGCCTTCATCAGCCTGGACCGGTTCCACGCCTACCTCGCCATTGTCCACGCCACCAA   553

Db   5221   TGTCCTCATCCTGGCCTTCATCAGCCTGGACCGGTTCCACGCCTACCTCGCCATCGCCACCACCAA   5280

Qy   554   CAGTCAAAGGCCAAGGAAACTGCTGCCTGAAAAGGCAGTCTATGTGGCGGTCTCGGATCCC   613

Db   5281   CAGTCAGAGCCCAAGGAAGGAAGCTGTGTCATCTTTTGCCGACTCTCATCTTTGCCTGGCTCTATGTTGGCTCATGTCTATGTGGCGGTCTCGGATCCC   5340

Qy   614   AGCCCTCCTCCTGACTATACCTGACTTCATCTTTTGCCAACG------------TCAG   673

Db   5341   TGCCCTCCTGCTGACTATTCCCGACTCATCTTTGCCAACG------------TCAG   5385

Qy   674   TCAGGGGGATGGACAGTACATCTGTGACCCGTTTACCCCGATAGCCTGTGATGGTGGT   733

Db   5386   TGAGGCAGATGACAGATATAATCTGTGACCCCAATGACTTGTGTGGGTGGTTGT   5445

Qy   686   CAGTACACTCTGTGACCGCCTTACCCCGATAGCCTGTGATGGTGGTGTTTCAATTCCA   745

Db   286   CAGTACACTGTGACCGCCTTACCCCGACAGCCTGTGATGGTGGTGTTTCCAGTTCCA   345

Qy   746   GCATATAATGGTGGGTCTCAGCTTCTTGCTGCTGCTGCCGCATCCTCCTCGTTACTGCATCAT   805

Db   346   GCACATCATGGTGGGTCTCATCGTCTCATCCTGTTACTGCATCAT   405

Qy   806   CATCCTAAGCTGTCACACTCCAAGGCCACCAGAAGCCGAAGCGCCTCAAGACAGT   865

Db   406   CATCCCCAAGCTGTCACACTCCAAGGCCACCAGAAGCCGAAGCGCCTCAAGACTACGGT   465

Qy   866   CATCCTCATCCTAGCTTCTTTGCCTGGCTGCTGCTGCCGTATATTGTGCCATATTCAGCAGCATCGA   925

Db   466   CATCCTTATCCTGGCTTCTTTGCCTGCTGCTGCCGTATCGGGATCAGCAGCATCGA   525

Qy   926   CTCCTTCATCCTTTGGGAGTCATCATCAAGCAAGGATGTGACTTCGAGAGCATTGTGCACAA   985

Db   526   TTCCTTCATCCTTTGGGAGGTCATCAAGCAAGGATGTGAGTTCGAGAGCGTCGTGCACRA   585

Qy   986   GTGGATCTCATCACAGAGGCCCTGCCTTCTTCCACTGTGCCTGAACCCATCCTCTA   1045

Db   586   GTGGATCTCCATCACGGAGGCCCTGCGCCTCTTCCACTGTGCCTGAACCCATCCTCTA   645

Qy   1046   TGCCTTCCTCGGGGCCAAGTCAAAAGTCTGCCCAGATGCACTCAACTCCATGAGCAG   1105

Db   646   CGCCTTCCTCGGGGCCAAATTCAAGAGCTCCGGCGCCAGCATGCACTCAATTCCATGAGCAG   705

Qy   1106   AGGCTCCAGCCTCCAAGATCCTTCCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCAC   1165

Db   706   AGGCTCCAGCCTCCAAGATCCTTCCAAAGGGAAACGGGGTGGACACTCTTCCGTCTCCCAC   765

Qy   1166   GGAGTCAGAATCCTCCAGTTTCACTCCAGCTAACCCTACGCTAACACATATATATAATAT   1225

Db   766   AGAGTTCAGAATCCTCCAAGTTTCACTCACGCTAACACTTACGCAAAGACATATATATAATAT   825

Qy   1226   ATATATATAT-------GATAAAGAACTTTTTATGTTACACATTTCCAGATAT   1275

Db   826   ATATATATATATATGACAGAACTTTTTTATGTTTACACATTTCCCAGATAT   885

Qy   1276   AAGAGACTGACCAGTCTGTACAGTTTTTTTTTTTTTTTAATTGACTGTTGGGAGTTTAT   1335

Db   886   AAAGACTGACCAATCTGTACAGTTTTTTTTTTTATTGACTGTTGGAGTTWANGTTTCTCYA   945

Qy   1336   GTTCCTCT-------AGTTTTGTGAGGTTTGACTTAATTATATAATAT-   1379

Db   946   GTTYYTGTGTGTGTGTGTGTGAGGTTTGACTTAATTTATATAAATATTGGTTTTTK   1005

Qy   1380   --TGTTTTTTGTTTGTTTTCATGTGAATGTGCTAGGCAGGACCGTCTGGCCAAGTTCTT   1437

Db   1006   TCTGTTTTGTCTGTTTTCACGTGAATGAGTGTCTAGGCAGGACCGTCTGGCCAAGTTCTT   1065

Qy   1438   AGTAGCTGTTTATCTGTGTCTGTGTGTAGGACTGTAGAACTGAAACTGAACATTCCA   1497

Db   1066   AGTCGCTGTGTGTCTGTGTGTAGGACTGTAGAGGAACGAACTGAACGCTCCA   1125

Qy   1498   GAATGTGTGTAAATTGAATAAAGCTAGCCGTGATCCTCAGCTGTTGCTGCATAATCTCT   1557

Db   1126   GAAATGTGTGTAAATCGGATAAAGCTAGAAGTGACCCT-AGCTGTCGCTGCATAATCTCT   1184

Qy   1558   TCATTCCGAGGAGCACCCCACCCCCCACCCCCCATTCTTAAATTGTTTGGT   1617

Db   1185   T------------CGCCCCGGCCCACCCCCGTTTCTTGTGAATTGTTTGGT   1218

Qy   1618   TATGTGTGTGATGGTTTGTTTTGGTGTTTGTTGTTGTTTTTTTTCTGT   1677

Db   1219   TGTGTGTGTG--------------GTTTCTCTGT   1239

Qy   1678   AAAAGATGGCACTTAAAACCAAAGCTGAAATGGCTAGAAATGCTGGGGTTTTTTTTG   1737

Db   1240   AGAAGATGGCACTTAAAACCAAAGCTTAAAACAAAGCTTGAAATGGT-ATAGAAATGCTGG--------   1287

Qy   1738   TTTGTTGTTTTTTTCAGTTTTCAAGAGTAGAGATTGACTTCAGTCCCTACACAAATGTACAGTC   1797

Db   5386   TGAGGCAGATGACAGATATAATCTGTGACCCCAATGACTTGTGTGGGTGGTTGT   5445

; ORGANISM: Rattus norvegicus
US-11-028-922A-4

Query Match 48.2%; Score 905.6; DB 7; Length 1050;
Best Local Similarity 91.6%; Pred. No. 7.5e-165;
Matches 975; Conservative 0; Mismatches 74; Indels 15; Gaps 1;

```
Qy  136 TGAGTATATACACTTCTGATAACTACTCTGAAGAAGTGGGGTCTGGAGACTATGACTCCA 195
        ||||| |||||||||| |||| |||||||| ||||| || ||| ||||||||||||||||
Db    2 TGGAAATATACACTTCGGATAACTACTCTCCGAGAGAGTAGGGTCTCGGAGACTATGACTCCA 61

Qy  196 ACAAGGAACCCTGCTTCCGGGATGAAAACGTCCATTCAATAGGATCTTCCTGCCACCA 255
        ||||||||||||||||||||||||||||| ||| |||||  |||||||||||||||||
Db   62 ACAAGGAACCCTGCTTCCGGGATGAAAACGAAAACTTCAACAGAATCTTCCTGCCACCA 121

Qy  256 TCTACTTCATCATCTTCTTGACTGGCATAGTCGGCAATGGATTGGTGATCCTGGTCATGG 315
        |||| |||||||||||||||||||||||||||| ||||||||||||| |||||||||||
Db  122 TCTATTTTATCATCTTCTTGACTGGCATAGTCGGCAATGGTTGGTGTAATCCTGGTCATGG 181

Qy  316 GTTACCAGAAGAAGCTAAGGACGCATGACGGACAAGTACCGGCTGCACCTGTCAGTGGCTG 375
        ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db  182 GTTACCAGAAGAAGCTGAGGACGCATGACAGACAAGTACCGGCTGCACCTGTCCGTGGCTG 241

Qy  376 ACCTTCCTCTTGTCATCACACTCCCCTTCTGGGCAGTTGATGCCATGGCCATGGTGACTACT 435
        ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  242 ACCTTCCTCTTGTCATCACACTCCCCTTCTGGGCAGTTGATGCCATGGCCATGGTGACTACT 301

Qy  436 TTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCG 495
        ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  302 TTGGGAAATTTTATGTGAAGGCTGTCCATATCATCTACACCGTCAACCTTACAGCAGTG 361

Qy  496 TTCTCATCCTGGCCTTCATCAGCCTGGACCGGTACCTCGCCATTGTCCACGCCACCAAACA 555
        ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db  362 TTCTCATCCTGGCCTTCATCAGCCTGGACCGGTACCTTGCCATTGTCCACGCCACCAACA 421

Qy  556 GTCAAAGGCCAAGGAAACTGCTGCTGAAAGGCAGTCTATGTGGGCGTCTGGATCCCAG 615
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  422 GCCAGAGCCGCGAGGAAGCTGCTGCTGAAAGGCGTCTATGTGGTCTCTGGATCCCCG 481

Qy  616 CCCTCCTCCTGACTATACCCTGACTTCATCTTGCCGACGTCAGCCAGGGGGACATCAGTC------ 675
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  482 CCCTCCTCCTGACTATCCCTGACATCATCTTCGCCGATGTCAGCCAGGGGGAC 534

Qy  676 AGGGGGATGACACAGGTACATCGTGACCGCCTTTACCCCGATAGCCTGTGATGGTGGTGT 735
        |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db  535 ------GGCAGTACATCGTGACCGCCTTTTGGGAGTCATCAAGGAGTCATCAAGAAGGAT 586

Qy  736 TTCAATTCCAGCATATAAATGTGGTCTCATCGTCATCCTCTCTGTT 795
        ||||||||||||||||||||||| |||||||||||||||||||||
Db  587 TTCATATTGATGTGTGTAGGCTGGTCTCATCGTCATCGTCATCCTGTTCCTCGTCTGTT 646

Qy  796 ACTGCATCATCATCCTAAGCTGTCACACTCCAAGGGCCACCAAGGGCCAAGCGCCCTCA 855
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  647 ACTGCATCATCATCCTCCAAGCTGTCACACTCCAAGGGCCACCAAGGGCCAAGGGCCCTCA 706

Qy  856 AGACGACAGTCATCCTCCTAGTTTCTTTGCCTGGCTCATCAAGGATGTGACTTCGAGAGCA 915
        |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db  707 AGACTACGGTCATCCTCATCCTTATCCTGGCTTCTTTGCCTGGCTCACCGTATTACGTGGGGA 766

Qy  916 TCAGCCATCAGCACTCCTTCCATCAGCATCACAGAGCCCTTCTTCCCACTGTTGCCTGAACC 975
        |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db  767 TCAGCCATCAGATTCCTTCATCCTTTCATCCTTTGGGAGTCATCAAGCAAGAAGGAGTTGAGAGCG 826

Qy  976 TTGTGCACAAGTGGATCTCCATCACACAGAGGCCCTTCTTCCCACTGTTGCCTGAACC 1035
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  827 TCGTTGCACAAGTGGATCTCCATCACACGGAGGCCCTTCTTCCCACTGTTGCCTGAACC 886

Qy 1036 CCATCCTCTATGCCTTCCTGGGGGCCAAGTTCAAAAGCTCTGCCCAGCATGCACTCAACT 1095
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  887 CCATCCTCTACGCCTTTCTGGGGGCCAAATTCAAGAGCTCCGCGCAGCATGCACTCAATT 946

Qy 1096 CCATGACGCAGAGGCTCCAGCTCAAGATCCTTTCCAAAGGAAAGCGGGGTGGACACTCTT 1155
        |||||||||||||||||||||||||||||||||||||||
Db ...
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RESULT 6
US-11-028-922A-4
; Sequence 4, Application US/11028922A
; Publication No. US2005271639A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Marc
; TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
; FILE REFERENCE: CCF-7019
; CURRENT APPLICATION NUMBER: US/11/028,922A
; CURRENT FILING DATE: 2005-01-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1050
; TYPE: DNA

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Db   947 CCATGAGACAGAGGCTCCAGCCTCAGATCTCTTTCCAAAGGGAAACGGGGTGGACACTCTT 1006

Db       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CCTTTTGGAGTCATCAAGCAAGGATGTGAGTTCGAGAGCGTCGTGCACAAGTGGATCTC 594

Qy  1156 CCGTCTCCACGGAGTCAGAATCCTCCAGTTTTCACTCCAGCTAA 1199
         |||||||||||||||||||||||||||||||||||||||||||
Db  1007 CCGTCTCCACAGAGTCAGAATCCTCAAGTTTTCACTCCAGCTAA 1050

Db       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CATCACGAGGCCCTCGCCTTCTTCGCCTTCTTCGCTGKTGCCTGAACCCATCCTCATGCCTCCT 1054

Db       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
         CATCACGGAGGCCCTCGCCTTCTTCGCCTTCTTCGCTGKTGCCTGAACCCATCCTCATGCCTCCT 654
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Query Match        47.4%;  Score 890.4;  DB 7;  Length 1400;
Best Local Similarity  79.4%;  Pred. No. 6.8e-162;
Matches 1227;  Conservative  20;  Mismatches 126;  Indels 173;  Gaps  10;

Qy   335 GAGCATGACGGACAAGTACCGGCTGCACCTGCTGAGTGGCTGACCTCCTCTTTGTCATCAC 394
         ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db     1 GAGCATGACAGACAAGTACCGGCTGCACCTGCTGAGTGGCTGACCTCCTCTTTGTCATCAC 60

Qy   395 ACTCCCCTTCTGGGGCAGTTGATGCTGGTACTTTGGGAAATTTTTGTGTAA 454
         ||||||||||||        ||||||||||||||||||||||||||||||||
Db    61 ACTCCCCTTCAG-------TGACGCGCATGCTGACTGGTACTTTGGGAAATTTTTATGTAA 114

Qy   455 GGCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCGGTTCTCATCCTGGCCTTCAT 514
         |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db   115 GGCTGTGCATATCATCTACACCGTCAACCTTTACAGCAGTGTTCTCATCCTGGCCTTCAT 174

Qy   515 CAGCCTGGACCGGTACCTCGCCATTGTCCACGCCACCAACAGTCAAAGGCCAAGGAAACT 574
         |||||||||||||||||||||||| || || ||||||||||||||||||||||||||||
Db   175 CAGCCTGGACCGGTACCTTGCCATTGTCCACGCCACCAACAGCCAGAGCGCGAGGAAGCT 234

Qy   575 GCTGGCTGAAAAGGCAGTCTATGTGGGCGTCTGATCCCAGCCCTCCTCCTGACTATACC 634
         ||||||||||||||                                         |||  ||
Db   235 GCTGGCTGAAAAGG----------------------------------------------C 249
         .

Qy   635 TGACTTCATCTTTGCCGACGACTGCAGCAGGGGACATCAGTCAGGGGGATGACAGGTACAT 694
         |||||||||||| |||||||||||||||||||||| ||||||||||||  |||||||||||
Db   250 CGACATCATCTTCGCCGATGTCAGCCGAGGGGGAC------------------GGCAGGTACACT 294

Qy   695 CTGTGACCGGCCTTTACCCCGATAGCCTGTGGATGGTGTTTCAATTCAGCATATAT 754
         ||||||||||||||||||||||||||  || |||||||||||||||||||||   ||
Db   295 CTGTGACCGGCCTTTACCCCGACAGCCTGTGGATGGTGTTCCAGTTCCAGCACACAT 354

Qy   755 GGTGGGTCTCATCCTGCCCGGGCATCGTCATCGTCATCCTGTTACTGCATCATCATCTCTAA 814
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   355 GGTGGGTCTCATCCTGCCCGGGCATCGTCATCGTCATCCTGTTACTGCATCATCATCTCCAA 414

Qy   815 GCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGAGCGCAAGAGCGCAAGACGACAGTCATCCTCAT 874
         ||||||||||| |||||||||||||||||||| ||||||||||||||||| |||||||||
Db   415 GCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGAGCGCAAGAGCGCAAGACTACGGTCATCCTTAT 474

Qy   875 CCTAGCTTTCTTTGCCTGCTGGCTGCCATATTATGTGGGATCAGCATCGACTCCTTCAT 934
         |||  ||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   475 CCTGGCTTTCTTTGCCTGCTGTACCGTATTACGTGGGGATCAGCATCGACTCCTTCAT 534

Qy   935 CCTTTTGGGAGTCATCAAGCAAGGATGTGACTTCGAGAGCATTGTGCACAAGTGGATCTC 994
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Qy  1055 CGGGGCCAAGTCAAAAGCTCTGCCCAGCAGCACTCAACTCCATGAGCAGGAGGGCTCCAG 1114
         |||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||||
Db  1055 CGGGGCCAAATTCAAGASSTCCGGCGAGCATGCAGCATCAATTCCATGAGCAGGAGGGCTCCAG 714

Qy  1115 CCTCAAGATCTTTCAAAGGAAAGCGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGA 1174
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   715 CCTCAAGATCCTTTCCAAAGGGAAAGCGGGGTGGACACTCTTCCGTCTCCACCAGAGTCAGA 774

Qy  1175 ATCCTCCAGTTTCACTCCAGCTACTAAACCCTTATGCAAAGACTTATATAATAATATATA 1234
         |||||||||||||||||||||| |||||||||||||||||||| ||||||| |||||||
Db   775 ATCCTCAAGTTTTCACTCCAGCTACACTTWCGCAAAGRCATATAAGRCATATATATATATA 834

Qy  1235 TAT------GATAAAGAACTTTTTTATGTTACACATTTTCCAGATATAAGAGACTGA 1285
         |||                                       ||||| ||||||
Db   835 TATATATATGMCAAAGACTTTTTTTATGTTTACACATTTTCCCAGATATAAAAGACTGA 894

Qy  1286 CCAGTCTTGTACAGTTTTTTTTTTTTTTTAATTGACTGTGTGGGAGTTTATGTTCCTCT-- 1343
         |||  |||||||||||||||||||:.||                       |||   |||
Db   895 CCAATCTTGTACAGTTTTTTTTTTTTTTTTATTGACTGTGGAGTTWATGTTTCTCTAGTTWTTGTGT 954

Qy  1344 -----AGTTTTGTGAGGTTTGACTTAATTTATATATAAATATTGTTTT----------TT 1387
         |||||||||||||||||||||:.|||||||||||||||||||||||||||CYGKTGKTT
Db   955 GTGTGTGTGTGTRAGGTTTGAYTTAATTTATATAAATATTGGKTTTTTTCYGKTGKTT 1014

Qy  1388 GTTTGTTCATGTGAATGAGCGTCTAGGCAGGACCTGTAGCCAAGTTCTTAGTAGCTGTT 1447
         |||||||| ||||| ||||||||||||||||||||||||||||||||||||||||:|
Db  1015 GTCTGTTTCACGTGAATGAGTGTCTCAGGCGAGGACCGTGCTGCCCAAGTTYTTAGTCGCTGTG 1074

Qy  1448 TATCTGTGTGTAGGACTGTAGAGAGGGAAGAAACTGAACATTCCAGAATGTGTGG 1507
         ||||||||||||||||||||||:|||:.||||| ||| |||||:|||||||||||
Db  1075 TGTCTGTGTGTAGGACTGTARAGAGTGTARAGGAAGAACTGAACGCTCCRGGAATGTGTGG 1134

Qy  1508 TAAATTGAATAAAGCTAGCCGTAGTCCTCAGCTGTTGCTGCATAATCTCTTCATTCCGAG 1567
         |||||| |||||||||||||   ||  |||:.||||||||||||| :||
Db  1135 TAAATCGGATAAAGTAGAGCTAGAAGTGACCCTCAGCTGTGCGCTGCATAATCTYT-------- 1185

Qy  1568 GAGCACCCCACCCCCCCCCCATTCTTAAATTGTTGGTTATGCTGTGT 1627
         |||                    ::|||||||||||||||||||||||
Db  1186 ------------YGCCCCGCCCACCCCGTTCCTGAATTGTTGGTTGGTTTTGGTTGTGCTGTGT 1228

Qy  1628 GATGGTTTGTTTGGTTTTTTTGTGTTTTTTTTCTGTAAAAGATGGC 1687
         ||||||||||                           ||||||||||
Db  1229 G-----------------------------------GTTTCTCGTARAAGATGGC 1249

Qy  1688 ACTTAAACCAAAGCCGAAAATGGTGGTAGAAAATGCTGGGGTTTTTTTTGTTGTT 1747
         |||||||||||||||||||||| ||||||||||||            |||||:||
Db  1250 ACTTAAAACCAAAGCCGAAAATGGT-ATAGAAAATGCTGG-------------GTTTTTTT 1294

Qy  1748 TTTTCAGTTTTCAAGAGTAGAGTAGCAGCTTCAGTCCTACAAAATGTACAGTCTTGTATTACA 1807
         ::|||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db  1295 YTTTCAGTTTTCAAGGGTGGATTGATTTCAGTACCTACAAAATGTACAGTCTTCTTGTATTATG 1354

Qy  1808 TTGTTAATAAAGTCAATGATAAACTTAAAAAAAAAAAAAAAAAA 1853
         ||||||||||||||||||||:.:||||||||||||||||||||
Db  1808 TTGTTAATAAAGTCAATGCAATGCTAAACTTRMAAAAAAAAAAAAAAAAAAAA 1400

Qy  1229 GATGGTTTGTTTGGTTTTTTTGTGTTTTTTTCTGTAAAAGATGGC 1249
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; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-112

Query Match   45.8%; Score 859; DB 6; Length 1225;
Best Local Similarity   83.3%; Pred. No. 6.8e-156;
Matches 1009; Conservative 0; Mismatches 180; Indels 22; Gaps 2;

Qy   136 TGAGTATATACACTTCTGATAACTACTCTGAAGAAGTGGGGTCTGGAGACTATGACTCCA 195
           ||||||||||||||||||||| ||||| ||||| ||||||||||||||||||||||||||
Db   16 TCAGTATATACACTTCGATCAGCAGCTCTGGGGTCTGGCAAGTGATGCCATGATGACTCCA 95

Qy   196 ACAAGGAACCCTGCTTCCGGGATGAAAAACGTCCATTTCAATAGGATCTTCCTGCCACCA 255
           |||||| ||||||| | ||||||| | |||||||| |||| |||||||||||||||
Db   96 TGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAATCTTCCTGCCACCA 155

Qy   256 TCTACTTCATCATCTTCTTGACTGGCAATGGCATAGTCGGCAATGGTGATCCTGGTCATGG 315
           |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   156 TCTACTTCCATCATCTTCTTAACTGGCAATTGTGGGCAATTGGTCATCCTGGTCATGG 215

Qy   316 GTTACCAGAAGAAGCTAAGGAGCACAGTGACGGACGACAAGTACCGGCTGCACCTGGCTG 375
           ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db   216 GTTACCAGAAGAAACTGAGAGAGTGACGGACGACAAGTACCGGCTGCACCTGGCGGCG 275

Qy   376 ACCTCCTCTTGTCATCACACTCCCCTTCTGGGCAGTTGATGCCATGGCTGACTGGTACT 435
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   276 ACCTCCTCTTGTCATCACACGTCCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTACT 335

Qy   436 TTGGGAAATTTTTGTGTAAGGCTGTCCAATATCATCTCACACTGTCAACCTCCTACAGCAGCG 495
           ||||||||||||||||||||||||||||||||||| || | ||||||||||||||||||
Db   336 TTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCGTCAACACTTCAACCTCTACACAGTG 395

Qy   496 TTCTCATCCTGGCCTTCATCAGCTGCGACCGGTACCTTCCACGCCACCAACA 555
           ||||||||||||||||||||||| |||||||||||||| ||||||||||||||
Db   396 TCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGCACGCCACCAACA 455

Qy   556 GTCAAAGGCCAAGGAAACTGCTGGCTGAAAAAGGCAGTCTATGTGGGCGTCTGAATCCCAG 615
           |||||||||||||||||||||||||| |||||||||| ||| |||| ||||| |||||||||
Db   456 GTCAGAGGCCAAGGAAGAAGTCGTGGCTGAAAAAGGTCGTCTATGTTGGCGTCTGGATCCCTG 515

Qy   616 CCCTCCTCCTGACTATACCTGACTTCATCTTTGCCGACGTCAGCCAGGGGACACTAGTC 675
           ||||||||||||||||||||||||||||||||| ||||||
Db   516 CCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCGACG------------TCAGTG 560

Qy   676 AGGGGGATGACAGGTACATCTGTGACCGGCCTTACCCCGATAGCCGTGTGATGGGTGTGT 735
           ||||||||||||| || ||| |||||||||||| ||||||||| ||||||| ||||||||
Db   561 AGGCAGATGACAGATATATCTGTGACCGCCTTCACCCCAATGACTTGTGGGTGGTTGTGT 620

Qy   736 TTCAATTCCAGCATAAATGGTGGTTCTCATCTCTGCCTGTT 795
           |||||||||| |||| |||||||| |||||||| ||||||||
Db   621 TCCAGTTTGCAGCACATCATGTTGCCCTGTATTGCTCGTGTCCTGCT 680

Qy   796 ACTGCATCATCATCCTGAAGCTCAAGGGCCACCAGAAGCCAAGGCCCTCA 855
           || |||| || |||||| ||||||||||||||||||||||||||||||||
Db   681 ATTGCATTATCATCCCAAGGCTCCAAGGGCCACCAGAAGCCAAGGCCCTCA 740

Qy   856 AGACGACAGTCATCCTCAGCTTTCTTCTTCGCTCGCTGTTGCTGCCTTACTACATTGGGGA 915
           ||||||||||||||||||| ||||||||| || |||| || |||| |||| |||||||| |
Db   741 AGACCACAGTCATCCTCATCCTCTGCTTTTCTGGGAGTCATCAAGCAAGATGCACTTCGAGAGCA 800

Qy   916 TCAGCATCGACTCCTTCATCCTTTGGGAGTCATCAAGCAAGATGCACTTCGAGAGCA 975
           |||||||||||||||||||||||| || |||| ||||||||||||||||||||||||
Db   801 TCAGCATCGACTCCTTCATCCTCTCCGGAAATCATCAAGCAAGATGGGCAGTTGACTGGTACT 860

RESULT 9
US-10-955-054A-121
; Sequence 121, Application US/10955054A
; Publication No. US2005026420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTXC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 1102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-121

Query Match   43.0%; Score 808; DB 6; Length 1102;
Best Local Similarity   85.9%; Pred. No. 4e-146;
Matches 914; Conservative 0; Mismatches 135; Indels 15; Gaps 1;

Qy   136 TGAGTATATACACTTCTGATAACTACTCTGAAGAAGTGGGGTCTGGAGACTATGACTCCA 195
           ||||||||||||||||||||| ||||| ||||| |||||||||||||||||||||||||||
Db   54 TCAGTATATACACTTCAGATAACTACACCACCCGAGGAAATGGGCTCAGGGACTATGACTCCA 113

Qy   196 ACAAGGAACCCTGCTTCCGGGATGAAAAACGTCCATTTCAATAGGATCTTCCTGCCACCA 255
           |||||| |||||||| | |||||| | |||||||| ||||| ||| |||||||||||||
Db   114 TGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAATCTTCAATGGTCATGG 173

Qy   256 TCTACTTCATCATCTTCTTGACTGGCAATGGCATAGTCGGCAATGGTGATCCTGGTCATGG 315
           |||||||| |||||||||||| ||||||| |||| |||||||||||||||||||||||||||
Db   174 TCTACTTCCATCATCTTAACTGGCAATGGCATTGGTGGGCAATGGTGTCATCCTGGTCATGG 233

Qy   316 GTTACCAGAAGAAGCTAAGGAGCACAGTGACGGACGACAAGTACCGGCTGCACCTGGCTG 375
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   234 GTTACCAGAAGAAACTGAGAGAAACTGAGAGCATGACGGACAAGTACCGGCTGCACCTGGTGCTG 293

Qy   376 ACCTCCTCTTGTCATCACACTCCCCTTCTGGGCAGTTGATGCCATGGCTGACTGGTACT 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   376 ACCTCCTCTTGTCATCACACTCCCCTTCTGGGCAGTTGATGCCATGGCTGACTGGTACT 435

; ORGANISM: Homo sapiens
US-11-121-086-8

Query Match   10.6%;   Score 198.4;   DB 7;   Length 246960;
Best Local Similarity   53.8%;   Pred. No. 1.7e-28;
Matches 456;   Conservative   0; Mismatches 386;   Indels   6;   Gaps   2;

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Qy     231  TTCAATAGGATCTTCCGCCACCATCATCATCTTCTTGACTGGCGATAGTCGGC  290
                |||||  ||||  |||  | |||||||
Db  120644  TTCAAGGCCGTGTTCGTGCCCGTACAGCCTCATCTTCCTCCTGGGCGGTGATCGGC  120703

Qy     291  AATGGATTGGTGATCCTGCTGGTGTCATGGGTTACCAGAGAAGCTAAGGAGCATGACGGACAAG  350
                ||||       |||   ||||||
Db  120704  AACGTCCTGGTGCTGGTGATCCTGGAGCGGCCAGACACGCGAGTTCCACGGAGACC  120763

Qy     351  TACCGGCTGCACCTGTCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCCTTCTGGGCA  410
                |||||      | ||||                      |||
Db  120764  TTCCTGTCCACCTGGCCGTGGCCCGACCTCCTCGTCGTCTTCATCTTGTGCCCTGCCGTG  120823

Qy     411  GTTGATGCCATGGCTGACTGGTACTTTGGTGAAGGCTGTCCATATCATC  470
                |||||      ||||||          |||
Db  120824  GCCGAGGGCTCTGTGGGCTGGTCCTGGGGACCTTCCTCGTGGGCTGGGTTGTGT  120883

Qy     471  TACACTGTCAACCTCACAGCAGCGGTTCTCATCGTGCCTTCATCAGCCTGGACCGGTAC  530
                |||| |||        |||  | |||||
Db  120884  CACAAGTCAACTTCTACTGCAGCCTGGCTGCTGGGCGTGGCCTGGACCGGCTAC  120943

Qy     531  CTCGCCATTGTCCACGCCACCAACAGTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCA  590
                ||||  ||||  ||||||   |||||||
Db  120944  CTGGGCCATTGTGTCCAGCGCGTCATGCCATGCCAGCCACGCGCCTCCTCCATCCACATC  121003

Qy     591  GTCATGTGGGCGTCTGGATCCCAGCCTCCTGGACTATACCTGACTTCATCTTTGCC  650
                |||       ||||                       |||
Db  121004  ACCTGTGGGACCATCTGGCTGGTGGGCTTCCTCCTGCCTTGCCTTGCCGCTTCTTTCGCC  121063

Qy     651  GACGTCAGCCAGGGACATCAGTCAGGGGATGACAGTTCAGGAGTACATCGTGACCGCCTTTAC  710
                ||||                       |||
Db  121064  AAAGTCAGCCAAGGCCATCACAACAACTCCCGCCACGTTGCACCTTCTCCCAAGAGAAC  121123

Qy     711  C---CCGATAGCCTGTGGATGGTGTTTCAATTCCAGCATATAATGGTGGGTCTCATC  767
                |         |||   ||||  |||||
Db  121124  CAAGCAGAAACGCATGCCTGTTCACCTCCGATTCCTCTACCATGTGGCGGGGATTCCTG  121183

Qy     768  CTGCCCCGGCATCGTCATCCTCCTGTTACTGCATCATCATCTCTAAGCTGTCACACTCC  827
                |||||      |||  | |||||
Db  121184  CTGCCCATGCTGGTGATGGGGCTGGTGCTACGTGGGGTAGTGCACAGGTTGCGCCAGGCC  121243

Qy     828  AA---GGGCCACCAGAAGCCAAGGCCTCAAGACAGCAGTCATCCTCATCCTAGCTTTC  884
                ||           |||   ||||
Db  121244  CAGCCGGCGCCCCTCAGCCGACAGAAAGGCAGTCAGGTGGCCATCCTGTGTGACAAGCATCTTC  121303

Qy     885  TTTGCCTGCTGGCTGTCACCCTACCACATCGTCATCTTCCTGGACACCCTGGGAGGCTGAAG  944
                |||||      ||||   | |||||
Db  121304  TTCCTCGCTGCTGGTGTCACCCAGTTCATCTTCCTGGACACCCTGGGCGAGGCTGAAG  121363

Qy     945  GTCATCAAGCAAGGAGGATGTGACTTCAGAGAGCATTGTGCACAAGTGGATCTCCATCACAGAG  1004
                ||| |       || |||   ||||
Db  121364  GCCGTGGACAATACCTGCAAGCTGAATGGCTCTCTCCCCGTGGCCATCACCATGTGTGAG  121423

Qy    1005  GCCCTGCCTTCTTCCACTGTGCCTGAACCCCATCCTCTATGCCTTCTATGCCTCCGGGGCCAAG  1064
                ||| |       ||||||
Db  121424  TTCCTGGGCCTGGCCCACCCTGCCTCCAACCCCATGCTGCTCTACACCTTTCGCCGGCGTGAAG  121483

Qy    1065  TTCAAAAG  1072
                ||| |||
Db  121484  TTCCGCAG  121491
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Db     294  ACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAAACTGGTACT  353
Qy     436  TTGGGAAATTTTGTGTAAGGCTGTCCATATCATCTACACTGTCAACCTCTACAGCAGCG  495
Db     354  TTGGGAAACTTCCTATGCAAGGCAGTCCATGTCATCTACACACAGTCAACCTCAACGCAGTG  413
Qy     496  TTCTCATCCTGGCCTTCATCAGCCTGGACAGCTGGTACCTCGGCGGTCCACGCCACCAACA  555
Db     414  TCCTCATCCTGTGGCCCTTCATCATCTGGACCGCTACCTGGCCTACCTCACAGCCACCAACA  473
Qy     556  GTCAAAGGCCAAGGAAACTGCTGGCTGAAAAGGCAGTCTATGTGGGCGTCTGGATCCCCAG  615
Db     474  GTCAGAGGGCCAAGGAAGCTGTTGGCTGAAAAGGTGTCTATGTTGGCGTCTGGATCCCCTG  533
Qy     616  CCCTCCCTCTGACTATACCTGACTTCATCTTTGCCGACGTCAGCCAGGGGACATCAGTC  675
Db     534  CCCTCCCGTCTGACTACTCATCTTTGCCAACG------------TCAGTG  578
Qy     676  AGGGGGATGACACAGGTACATCTGTGACCGGCCTTTACCCCGATAGCCTGTGTGGATGTGGTGT  735
Db     579  AGGCAGATGACAGAGATATCTGTGACCGGCTTCTACCCCAATGACTTGTGGGTGGTTGTGT  638
Qy     736  TTCAATTCCAGCATATAAATGGTGGTCTCATCCTGCCCGGCATCGTCATCCTCCTGTGTT  795
Db     639  TCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTTATCCTGTATTGTCATCCTGTGTTCCTGCT  698
Qy     796  ACTGCATCATCATCCTAAGCTGTCACACTCCCAAGGGCCACCAGAAGCGCAAGGCCCTCA  855
Db     699  ATTGCATTATCATCCTCCAAGCTGTCACACTCCCAAGGGCCACCAGAAGCGCAAGGCCCTCA  758
Qy     856  AGACAGACAGTCATCCTCATCCTAGCTTTCTTTTGCCTGCTGGCTGCCATATTATGTGGGGA  915
Db     759  AGACCACAATCATCCCCATCCTCTGGCTTTCTTTCTTCGCCTGTGTGCCTTACTACAGATTGGGA  818
Qy     916  TCAGCATCGACTCCTTCATCCTTTTTGGGAGTCATCAAGGAAGGATGTGACTTCGAGAGCA  975
Db     819  TCAGCATCGACTCCTTCATCCTTTTTGGGAGCCAAGGGTGTGAGTTTGGAAGACA  878
Qy     976  TTGTGCACAAGTGGATCTCCATCACAGAGGCCCTGCCCTTCTTCCCGCCTGTTGCCTGAACC  1035
Db     879  CTGTGCACAAGTGGATTTCCATCACGGAGCCCAGCTTTCTTCCTCCACTGTGTCTGAACC  938
Qy    1036  CCATCCTCTATGCCTTCGGGCCCAAGTTCAAAAAGTCTGCCCAGCATGCACTCAACT  1095
Db     939  CCATCCTCTATGCCTTTGGAGCCAAATTAAAACCTGCCCAGCACGCACTCACCT  998
Qy    1096  CCATGAGCAGAGGCTCCAGCCTCCAGAGATCCTTCCAAAGGAAGCGGGGTGGGACACTCTT  1155
Db     999  CTGTGAGCAGAGGGTCCAGCCTCCAAGATCCTCCAAAGGAAAGCGGAGGCGGGACATTCAT  1058
Qy    1156  CCGTCTCCACGGAGTCAGAATCCTCCAGTTTCACTCCAGCTAA  1199
Db    1059  CGTTTCCACTGAGTCTCGAGTCTTCAAGTTTCACTCCAGCTAA  1102
```

RESULT 10
US-11-121-086-8
; Sequence 8, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 246960
; TYPE: DNA

RESULT 11
US-11-136-527-153
; Sequence 153, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

```
;   APPLICANT: Wyeth
;   APPLICANT: Mounts, William M
;   TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;   FILE REFERENCE: 031896-041000 (AM101086)
;   CURRENT APPLICATION NUMBER: US/11/136,527
;   CURRENT FILING DATE: 2005-05-25
;   PRIOR APPLICATION NUMBER: US 60/574,294
;   PRIOR FILING DATE: 2005-05-26
;   NUMBER OF SEQ ID NOS: 362830
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 153
;   LENGTH: 1680
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-153

Query Match          9.4%;    Score 176.4;   DB 7;   Length 1680;
Best Local Similarity   50.2%;    Pred. No. 6.3e-25;
Matches  457;   Conservative  5;   Mismatches  436;   Indels  12;   Gaps  1;

Qy    161  CTCTGAAGAAGTGGGTCTGGAGACTATGACTCCAACAAGGAACCTGCTTCCGGGATGA  220
Db    226  CTACGATTATGGGAAAAMRAAARMRAMWMTCTGACTCCCCGCCTGCCCACAGGACTT  285

Qy    221  AAACGTCCATTCAATAGGATCTTCCTGCCACCATCTACTTCATCTTCTTGACTCG  280
Db    286  CAGCCTGAACTTTGACAGAACCTTCCTGCCAGTCCTACAGCCTCCTCTTTTTGCTGGG  345

Qy    281  CATAGTCGGCAATGGATTGGTGATCCTGGTCATGGGTTACCAGAAGAAGCTAAGGAGCAT  340
Db    346  GCTGCTAGGCAATGGGCAGTGGCTGCTGCTACTGAGCCACGCGCAGTCCCTGAGCAG  405

Qy    341  GACGGACAAGAAGTACCGGCCTGCACCTGTGCTGCTGACCTCCTCTTTGTCATCACACTCCC  400
Db    406  CACAGACACCTTCCTCGCTCACCTGGCGTGTGGCCGATGGTACTGCTGGTACTAACCCTCCC  465

Qy    401  CTTCTGGGCAGTTGATGCCATGGCTGACTGGTACTTTGGGAAATTTTTGTGTAAGGCTGT  460
Db    466  ACTGTGGGCAGTAGATGCTGCGCCCAGTTGGGTTTTCGGCGTCTGCAAAGTGGC  525

Qy    461  CCATATCATCTCACACGTGTCAACCTCTACAGCAGGGTTCTCATCCTGGCCTTCATCAGCCT  520
Db    526  AGGTGCCCCTGTTCAACATCAACTTCTACGCGAGGGCCTTCCTGGCCTTGTATAAAGCTT  585

Qy    521  GGACCGGTACCTCGCCATTGTCCACGCCACCAACAGTCAAAGGCCAAGGAAAACTGCTGGC  580
Db    586  TGACCGGTACCTGGCAGCATAGTGCATGCCACCACCCAGATCTACCGGGGACCCCTGGGTACG  645

Qy    581  TGAAAAGGCAGTCTATGTGGGCGTCGGAATCCCAGCCCTCCTCCCTGACTATACCTGACTT  640
Db    646  TGTAGCCCTGCACTTGTCACTTGTGGGGTCTCGTGTGTCTCTTTGCCCTCCCAGATTT  705

Qy    641  CATCTTTGCCGACGTCAGCCAGGGGGAGACATCAGTCAGGGGATGACAGTACATCTGTGA  700
Db    706  CATCTTCCTGTCAGCCAGCCA-----------TGATCAGCGCCTCAATGCCACCCATTG  753

Qy    701  CGGCCTTTACCCCGATAGCCTGTGGATGGTGTTCAATTCCAGCATAATAATGGTGGG  760
Db    754  CCAGTACAACTTCCCACAGGTGGGTCGGACTGCTCTCGGTGTACTGGCTAGTGCGTGG  813

Qy    761  TCTCATCCTGCCCCGCATCGTCATCCTCTCCGTGATGGTGTTCTACTGCATCATCTCTCTAAGGCTGTC  820
Db    814  TTTCCTGATGSCCCTCCTAGTCATTGCCTATGCGCTATGCCCATATGCCTGGCTGTCGCTGCT  873

Qy    821  ACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTAGC  880
Db    874  GGTCTCCAGAGGCCCAGAGCGCGCTTTCGAGCTATGAGGCTAGTGGTGGTGGTGGCC  933

Qy    881  TTTCTTTGCCTGGGCTGCTGCCATATTATGTGGGATCAGCATCTCCTTCATCCTTTT  940
Db    934  CTTTGCCGTCTGCTGGACCCCCTATCACCTGGTGTTAGTGATATCCTTATGGACGT  993

Qy    941  GGGAGTCATCAAGCAAGGAGATGCACTTCGAGAGCATTGTGCACAAGTGGATCTCCATCAC  1000
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Db    994  GGGAGTTTGGCCCGCAACTGTGGTGCGAGAAAGGCATGTGGACTGGACGGGCTAGCCAAGTCAGTCAC  1053
Qy   1001  AGAGGCCCTGCCTTCTTCCCACTGTTGCCTGAACCCCATCCTCGAACCCTTCCTCGGGGC  1060
Db   1054  CTCAGGCATGGCATGGCTACATCCACTGCTGCCTCAATCCACTGCCTCATCATGCCTTTGTGGGAGT  1113

Qy   1061  CAAGTTCAAA  1070
Db   1114  GAAGTTCAAA  1123
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RESULT 12
US-11-136-527-2373
;   Sequence 2373, Application US/11136527
;   Publication No. US20050287570A1
;   GENERAL INFORMATION:
;   APPLICANT: Wyeth
;   APPLICANT: Mounts, William M
;   TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;   FILE REFERENCE: 031896-041000 (AM101086)
;   CURRENT APPLICATION NUMBER: US/11/136,527
;   CURRENT FILING DATE: 2005-05-25
;   PRIOR APPLICATION NUMBER: US 60/574,294
;   PRIOR FILING DATE: 2005-05-26
;   NUMBER OF SEQ ID NOS: 362830
;   SOFTWARE: PatentIn version 3.2
;   SEQ ID NO 2373
;   LENGTH: 1324
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-11-136-527-2373

Query Match          9.3%;    Score 175;   DB 7;   Length 1324;
Best Local Similarity   52.2%;    Pred. No. 1.1e-24;
Matches  441;   Conservative  0;   Mismatches  395;   Indels  9;   Gaps  2;

Qy    222  AACGTCCATTCAATAGGATCTTCCTGCCACCATCTACTTCATCTTCTTGACTGGC  281
Db    255  AACCTAGATATCAACAGGTATGCTGTCATATACGTTCGTGTGTGTGCATTGCTGAGT  314

Qy    282  ATAGTCGGCAATGGATTGGTGATCCTGGTCATGGGTTACCAGAGAAGAAGCTAAGGAGCATG  341
Db    315  CTCGTGGGGAACTCCCTGGTGATGCGTGGTCATCTGTAGTGCAAATCGAAGCACCTGCTCTGTT  374

Qy    342  ACGGACAAGTACCGGCCTGCACCTGTCAGTGGCTGCTGACCTCCTCTTTGTCATCACACTCCCC  401
Db    375  ACCGACGTCACCTGTCGAACCTGGCCATTGCTGCTGACCTGTCGTCTTTGCCCTGCCT  434

Qy    402  TTCTGGGCAGTTGATGCCATGGCTGACTGGTACTTTGGGGAAATTTTTGTGTAAGGCTGTC  461
Db    435  GTCTGGGCTGCATCTAAAGTAAATGATGGATTTTGGCTCATTCCTGTGCAAGGTATTC  494

Qy    462  CATATCATCTCACACGTGTCAACCTCTACAGCAGGCCTTCATCATCAGCCTG  521
Db    495  TCGTTCCTGCAGGAGATTACCTTCTACAGTGTTCGTGTGCTAGCCTGTCATCAGCATG  554

Qy    522  GACCGGTACCTCGCCATTGTCCACGCCACCAACAGTCAAAGGCCAAGGAAACTGCTGGCT  581
Db    555  GACCGCTACCTGGCCATCGTCCACGCCCACCAAGTACACTGATACACTTGATCCAGAAGAGACACTTG---  611

Qy    582  GAAAAGGCAGTCTATGTGGGCGTCGGATCCCAGCCCTCCTCCTGACTATACCTGACTTC  641
Db    612  GTCAAGTTGTGTGCATCACCATGTGGTTTCTCTCACTAGTTCTGTCCCATCTTC  671

Qy    642  ATCTTTGCCGACGTCAGCCAGGGGACATCAGTCAGGGGATGACAGGTACATCTGTGAC  701
Db    672  ATTCTTCGGACTACTGTTAAGGCAAACCCTTCTCTGCTCGTATGAGAATAAGGT  731

Qy    702  CGGCCTTTACCCCGATAGCCTGTGGATGGTGTTCAATTCCAGCATAATAATGTGGGT  761
Db    732  AATAATACATCCAA------GTGGAGGGGTGTACTGGTACTGGCCGCATCCTGCCTCAGACCTATGGC  785
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Qy    762 CTCATCCTGCCCGGCATGCTCATCCTCGTACTGCATCATCATCCTAAGCTGTCA 821
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Db    786 TTCCTCCTGCGCGTGCTCATCATGCTGTTCTGCTATGGGTTCACACTGGCACGCTCTTT 845

Qy    822 CACTCCAAGGGCACCAGAGAGGCCAAGGCCTCAGAGACAGTCATCTCATCCTAGCT 881
          ||||    ||||  |||||
Db    846 AAGGCCCACATGGGGCAGAAGCACCGGGCACCCATGCGGGTCATCTTGCGTGGTCCTCGTC 905

Qy    882 TTCTTTGCCTGCTGGCTGCCATATATGTGGGATCAGCAGCATCGACTCCTTCATCCTTTTG 941
          ||||  |||||   ||||||  |||
Db    906 TTCCTGCTTCGTGGCTTGCTCCTGTTCCTACAGACACCCATGAGAACC 965

Qy    942 GGAGTCATCAAGCAAGGATGTGACTTCGAGAGACATTGTGCACAAGTGGATCTCCATCACA 1001
          |||  ||||  ||||||
Db    966 AAGCTGATCAAGGGAGACCTGTGAACGCCAGAACCAGAATTAACAAAGCTTGGAAGCTACT 1025

Db   1002 GAGGCCCCTGCCTTCTTCCACTGTTGCTGGCCCTGCTGAACCCATCCTCATGCCTTCCTCGGGGGGGC 1061
          |||||
Db   1026 GGATTCTTGGCTTCCTCCACAGCTGTCTTAACCCCATCCATCATGCCTATGGGTTTATTGGCCAG 1085

Qy   1062 AAGTT 1066
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Db   1086 AAATT 1090
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RESULT 13
US-10-750-185-54253/c
; Sequence 54253, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;   APPLICANT: MMI GENOMICS, INC.
;   APPLICANT: DeNISE, Sue K.
;   APPLICANT: KERR, Richard
;   APPLICANT: ROSENFELD, David
;   APPLICANT: HOLM, Tom
;   APPLICANT: BATES, Stephen
;   APPLICANT: FANTIN, Dennis
;   TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;   FILE REFERENCE: MMI1100-2
;   CURRENT APPLICATION NUMBER: US/10/750,185
;   CURRENT FILING DATE: 2003-12-31
;   PRIOR APPLICATION NUMBER: US 60/437,482
;   PRIOR FILING DATE: 2002-12-31
;   NUMBER OF SEQ ID NOS: 64922
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 54253
;   LENGTH: 1433
;   TYPE: DNA
;   ORGANISM: Bovine 1986880583235
US-10-750-185-54253

Query Match   9.1%;   Score 170; DB 6; Length 1433;
Best Local Similarity 51.4%; Pred. No. 1e-23;
Matches 448; Conservative 0; Mismatches 415; Indels 9; Gaps 2;

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Db    859 GTGAACTTCTACAGTGGCATCTTCTTCATCCAGCTGCATGAGCCTGCAGCAGTACTGGAG 800
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Qy    537 ATTGTTCACGCCACCAAACAGTCAAGGACCAAGGAAACTGTCGGCTGAAAAGGCAGTCTAT 596
          |||||||            ||||
Db    799 ATTGTTCTGCGCTGGCCTCGGCCCTACCACCGACTGAGGACCCGAGCCAAGAGCCTGTTGCTTGCA 740

Qy    597 GTGGGCGTCTGGATCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTTGCCGACGTC 656
          ||||            ||||||||
Db    739 GCCAGTGTGTGGGCTATGGCCCTGCTGTGTCTTCCATTCCTGACATGTCTTT-----GTG 686

Qy    657 AGCCAGGGGACATCAGTCAGGGGGATGACAGTACATCTGTGACCGCTTTACCCGAT 716
          ||||        |||||||
Db    685 AGGACGCCATGAGAACTCCCCGGGGTGTGGAGTGTCATGCAGATTTGGGGACATGGG 626

Qy    717 AGCCTGTGGATGGTGTGTTTCAATTCAGCATATAATGGTGGTCTCATCCTGCCCGGC 776
          ||||||            |||||||
Db    625 ACCATCTGGAAGCTCTTCCTGCCGCTTCCGCTTCTGACTCGCCAAGTCTTTGGGGAC 566

Qy    777 ATCGTCATCCTCTCGTTACTGCATCATCTCTCAAGCTGTCACACTCCAAGGGCCAC 836
          ||||||
Db    565 CTTGCCATGACTTCTTCTACTCCCGCATTGGCTGTGTGCTGTGAGTCTGGAGTGGTG 506

Db    837 CAGAAGCGCAAGGCCCTCAAGACGACAGTCATCCTCATCCTAGCTTCTTCTTGCCTGCTGG 896
          ||||||
Db    505 GGCCAGAGCGCGGGCCCTGAGGATGGCCGTAGCTCGGTGGTGGCCTTCTCTTTGTGCTGTGG 446

Qy    897 CTGCCATATTATGTGGGGATCAGCATCAGCATCGACTCCTTTTGGGAGTCATCAAGCAA 956
          |||| ||            ||||
Db    445 TTCCCGTACAATCTCACCTTGTTCCTGCACTCGCTGCTGGACCTCCAAGTCTTTGGGGAC 386

Qy    957 GGATGTGACTTCGAGAGACATTGTGCACAAGTGGATCTCCATCACAGAGGCCCTCGCCTTC 1016
          ||||
Db    385 TGCAGGGTCAGCCAGCAC---CTGGACTATGCGGCTGCAGGTGACGGAGCAGCATCGGCCTTC 329

Qy   1017 TTCCACTGTTGCCTGAACCCCATCCTCATCCTATGGCCTTCCTCCTGCGGGGCCAAGTTCAAAAGCTCT 1076
          ||||
Db    328 CTGCACTGCTGCTTCACCCCGTCCTCCTCGTGCCTCTTCTCCAGCCACCGCTTCCGCCAGTAC 269

Qy   1077 GCCCAGCATGCACTCAACTCAACTTCCATGAGCAGAGG 1108
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Db    268 CTCAAGGCCTTTCCTGGCCACTGTGCTCAGAAG 237
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RESULT 14
US-10-750-623-54253/c
; Sequence 54253, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;   APPLICANT: MMI GENOMICS, INC.
;   APPLICANT: DeNISE, Sue K.
;   APPLICANT: KERR, Richard
;   APPLICANT: ROSENFELD, David
;   APPLICANT: HOLM, Tom
;   APPLICANT: BATES, Stephen
;   APPLICANT: FANTIN, Dennis
;   TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;   FILE REFERENCE: MMI1100-1
;   CURRENT APPLICATION NUMBER: US/10/750,623
;   CURRENT FILING DATE: 2003-12-31
;   PRIOR APPLICATION NUMBER: US 60/437,482
;   PRIOR FILING DATE: 2002-12-31
;   NUMBER OF SEQ ID NOS: 64922
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 54253
;   LENGTH: 1433
;   TYPE: DNA
;   ORGANISM: Bovine 1986880583235
US-10-750-623-54253

Query Match   9.1%;   Score 170; DB 6; Length 1433;
Best Local Similarity 51.4%; Pred. No. 1e-23;
Matches 448; Conservative 0; Mismatches 415; Indels 9; Gaps 2;

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; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4249
;    LENGTH: 1400
;    TYPE: DNA
;    ORGANISM: Rattus norvegicus
US-11-136-527-4249

Query Match          9.0%;     Score 168.6; DB 7; Length 1400;
Best Local Similarity 51.0%;   Pred. No. 1.9e-23;
Matches  433;  Conservative  0;  Mismatches 404;  Indels  12;  Gaps  1;

Qy    222 AACGTCCATTCAATAGGATCTTCCTGCCACCATCTACTTCATCATCTTCTTGACTGGC 281
          ||||| |||| |||   ||| ||||  || ||||||||  | || |||| |||||||||
Db      7 AGCCTGAACTTTGACAGAACCTTCCTGCCAGTCCTCTCACAGCCTCCTCCTTTTGCTGGGG 66

Qy    282 ATAGTCGGCAATGGATTGGTGATCCTGGCATGGTTACCAGAGAAGCTAAGGAGCATG 341
          |||  |   | ||    |||| || || ||  | ||||| ||| || ||  ||||| |||
Db     67 CTGCTAGGCAATGGGGCAGTGGGCTGTGCTACTGAGCCAGCCGCACTGCCCTGAGCAGC 126

Qy    342 ACGGACAAGTACCGGCCACTCCTTGTCATCAGTGGCTGACCTCCTCTTTGTCATCACACTCCCC 401
          | || || || |  |  || ||||||| ||||  |||   |   ||| |||||||| ||| ||
Db    127 ACAGACACCTTCCTGCTCCACCTGGCGCTGTGTGCCCGATGACTGCTGGTACTGACCCTCCCA 186

Qy    402 TTCTGGGCAGTTGATGCCATGGCTGACTGTACTTTGGGAAATTTTGTGTAAGGCTGTC 461
          ||   |||||| |  | ||||| |  |   |||||   |||  ||  |||| ||||  |
Db    187 CTGTGGGCAGTAGATGTCTGCTGCCCAGTGGGTTTTCGGCTGCCTCTGCAAAGTGGCA 246

Qy    462 CATATCATCTACACTGTCAACCTCTACAGCAGCCTTCTCATCCTGGCCTTCATCAGCCTG 521
          ||| ||| || |  ||| ||| |  ||| ||||| |  | |||| |  || |||||| ||
Db    247 GGTGCCCTGTTCAACATCAACTTCTACGGCAGGGCCTTCTGGCTTGGCCGTATAAGCTTT 306

Qy    522 GACCGGTACCTCCGCCATTGTCTGTGATGGCGTCTGGATCCCAGCCCTCCTCGACTATACCTGACTTC 581
          ||| || ||| | || | | ||| |  | | ||| ||   |  |  ||  || |  |||||||  |
Db    307 GACCGCTACCTGGGCATAGTCACCACCACCAGAGGGACCCCGCCAGGGGACCCCTGGGTACGT 366

Qy    582 GAAAAGGCAGTCTATGTGGGCGTCTGGATCCCAGCCCTCCTCGACTATACCTGACTTC 641
          | |||| |||  ||||||| |  ||||   |  | |  ||||  |||   | |||| |
Db    367 GTAGCCTCACCTGCATTGTGTGGGGATGACAGCAGCAGCGGATGACAGGTACATCTGTGAC 426

Qy    642 ATCTTTGCCGACGTCAGCAGCGTCTCCAGAGCTCACCATCAGCCTGATGACAGCGGTGTGG 701
          ||| || ||  |  ||||| |   ||  | ||  |  | ||||   ||  | || ||||||
Db    427 ATCTTCCTGTCAGCGACCATGATCAGCGCCTCAATG--------CCACCCATTGC 474

Qy    702 CGCCTTTACCCCGGATAGCCTGTGGATGGTGGACTTTCAATTCCAGCATATAATGGTGGT 761
          |||||| |||| || |||| |||| | || || ||||||  |||||||| | |||| |||
Db    475 CAGTACAACTTCCCACAGGTGGGTCGGACTGGCAGTGTGCTCAGCAGTAGTAGTGCTGGT 534

Qy    762 CTCATCCTGCCGCCATCGTCATCTCTCGTTACTGATCATCATCATCCTGGCTGTGTGCTG 821
          || ||||  | | || | | |   ||||    |||| | || ||||   ||  | ||||||
Db    535 TTCCTGATGCCCCTTCCGTAGTCATGGCTCATCATGCCGATGACGGACAGTGTCAGCTTCA 594

Qy    822 CACTCCAAGGCCACCAGAAGCGCAAGGCCACGACTGGTGGTGGTGGCC 881
          ||  ||||| || ||||| || ||||  || | ||||||||||||||||
Db    595 GTCTCCAGAGGCCAGAGGCGCTTTCGAGTCATGAGGCCGTCAGTGGTGGTGGTGGCC 654

Qy    882 TTCTTTGCCTGCTGGTGCTGCCATATTATGTGGGGATCAGCATCAGCTCCTTTG 941
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Db    655 TTTGCCGTCTGCTGCTGGACCCCGTCTGTGTTAGTAGTGGATATCCTTATGGACGTG 714

Qy   1002 GAGGCCCTGCCTTCTTCCACTGTTGCTGCCATCCTCATGCCTCT 1061
          |||||| | |   || |   || |||||||||| || | || |
Db    775 TCAGGCATGGCTACATGCGCCTACATGCCATCCAATCCACTGCTTCAATCCACTGCTGCTCAATCCACTGCTGCTCATGCCTCTCTATGCCTTTGTGGGAGTG 834

Qy   1062 AAGTTCAAA 1070
          |||||||||
Db    835 AAGTTCAAA 843
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Qy    237 AGGATCTTCCTGCCACCATCTACTTCATCATCTTCTTGACTGGCATAGTCGGCAATGA 296
          || |||||||  |  |  | ||    | ||||| |||| |  |  ||
Db   1099 AGAGTCTTTCTACCTGTCTTCTACAGCCTGATCTTTGTCTGCTGGGGCCCTGTTGAAACCTC 1040

Qy    297 TTGGTGATCCTGGTCATGGGTTACCAGAGAAGCATGAAGGACAAGTACCGG 356
          |||| |    | || ||| || ||| || | |  |   ||| ||  || ||
Db   1039 CTCCTCCTAGCCGGTCTTCGTCCGGTTCCGGTTCCCGGATGCAGAGACGGATGACCGAGACCTATCTG 980

Qy    357 CTGCCACCTGTCAGTGGCTGGCTGACCTCCTTTGTCATCACACTCCCCTTGTCTGGGCAGTTGAT 416
          ||  | ||  | | | |  | |  | |   |||||||||| || |   | | ||||||||  ||
Db    979 CTGAACCTGGCCATCTCCAACTCCTGTTGTGTGGTGCACACTGCCCTTCTGGGGCATCTCT 920

Qy    417 GCCATGGCTGACTGTACTTGGGAAATTTTTGTGTAAGGCTGTCCATATCATCTACACT 476
          |||||  | |   | ||||||||  |||   | | || |   |||| | | | || | |
Db    919 GTGGCATGGCATTGGGTCTTATGCAAGGTGTTGGTTCAAGGTGTGTGAGCACCCTCTATACC 860

Qy    477 GTCAACCTCTACAGCAGCCTGGCCTTCATCAGCCTGGACCGGTACCTCCGC 536
          ||||| ||| |  | || ||| |  || | |  |||||| || |||  | |
Db    859 GTGAACTTCTACAGTGGCATCTTCATCAGCCTGATCAGCCTGGACAGTACCTGGAG 800

Qy    537 ATTGTCCACGCCACCAACAGTCAAGGCCAAGGAAACTGCTGGCTGGCAGTGCAGTCTAT 596
          |||| |  |  ||||||| ||||| ||||  | |||  ||||   || ||| || ||||
Db    799 ATTGTCTGCCGCTCGGCGTCCACCACTGCCTCCGCCCTGCCTGTTGCTTGCA 740

Qy    597 GTGGGCGTCGGATCCCAGCCCTCCTCGACTATACCTGACTTGCGACGTC 656
          |||  | | |||   | | |  |||| |  | | ||  |    || |  ||
Db    739 GCCAGTGTGTGGGGATGGCCCTGCCCGGGGCGGGGGTCATGCCTATGCTCCGGGTCTCTTT------GTG 686

Qy    657 AGCCAGGGGACAATCAGTCAGGGGGATGACAGCAGCCCTTTACCCCGAT 716
          |||||||||||| | || ||  | | || | |   | |  |||||| ||
Db    685 AGGACGCATGAGAACTCCCCGGCGTGTGGGTCATGCGTGGGGACATGGG 626

Qy    717 AGCCTGTGGATGGTGGTGTTTCAATTCCAGCATATAATGGGGTCTCTCATCCTGCCCGGC 776
          |||||||| |||||| |||||||| |||||| | | || || ||  ||  | | || ||
Db    625 ACCATCTGGAAGCTCTTCACCTTGTTCCTGCCGCTTCCAGACAGAACCTCTGGGGTTTCTCTCCTCTC 566

Qy    777 ATCGTCATCCTCTCTGTTACTGCATCATCATCTCTAAGCTGTCAAGGGCCAC 836
          || | || |||| ||  | | ||||  | | ||||| | || |  | ||||
Db    565 CTTGCCATGATCTTCTTCACTCCGTGTCTGGTGAGTCTGGAGGCCCCG 506

Qy    837 CAGAAGCGCAAGGCCCTCAAGACAGACAGCATCATCCTAGCTTTCTTTGCCTGTCTGG 896
          | |||| | |||  || | ||| |  | ||||||||| ||  ||  || |  ||| |||
Db    505 GGCCAGAGGCGGGCCCTGAGGAGTGCCGTAGCTGTGGCCTTCTTGTGCTGTGTGG 446

Qy    897 CTGCCATATTATGTGGGGATCAGCAGCAGCACGACTGCTCCTTCATCCTTTTGGGAGTCATCAAGCAA 956
          || || | | || | ||| |||| |||| |  | ||  ||||| | |||  ||| |||||  | |||
Db    445 TTCCCGTACAATCTGTCCGCTGGATCTCCGACTGCGAAGTCGCAGTCTTTGGGGAC 386

Qy    957 GGATGTGACTTCGAGAGACTTCCATCACAGAGGCCCTGCCTTCC 1016
          ||||  || ||| |||| |  | ||  |  |  | |   || ||
Db    385 TGCAGGGTCAGCAGCCAGCAC---CTGGACTATGCGCTACTGCTGGGGGGACATCGCCCTTC 329

Qy   1017 TTCCACTGTTGCTGACCCATCCTCTATGCCTTTCCTGGGGGCCCAAGTTCAAAAGCTCT 1076
          |||| ||  |||||  || ||| | |  |||| |||  |||  || |  |||||| |
Db    328 CTGACTGCTGCTTCACCCCGTCTTCTCTACGCCCTTCTCCAGCCACCACCGCTTCCGCCAGTAC 269

Qy   1077 GCCCAGCAGCACTCAACTCCATGCAGCAGAGG 1108
          |||||||| || |||| |||||| |||  |||
Db    268 CTCAAGGCTTTCCTGGCCACTGTGCTCAGAAG 237
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RESULT 15
US-11-136-527-4249
; Sequence 4249, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
;   APPLICANT: Wyeth
;   APPLICANT: Mounts, William M
;   TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;   FILE REFERENCE: 031896-041000 (AM101086)
;   CURRENT APPLICATION NUMBER: US/11/136,527
;   CURRENT FILING DATE: 2005-05-25
;   PRIOR APPLICATION NUMBER: US 60/574,294
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us-09-367-052-1.rmpbn

Thu Jan 12 11:12:42 2006

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OM protein - nucleic search, using frame_plus_p2n model

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

Run on: January 10, 2006, 20:54:02 ; Search time 285 Seconds
(without alignments)
2239.104 Million cell updates/sec

Title: US-09-367-052-2
Perfect score: 1867
Sequence: 1 MEPISVSIYTSDNYSEEVGS.........KRGGHSSVSTESESSSFHSS 359

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Score	Query Match	Length	DB	ID	Description
1	1678.5	89.9	1059	3	US-09-647-501-1	Sequence 1, Appli
2	1678.5	89.9	1225	3	US-09-016-434-1235	Sequence 1235, Ap
3	1678.5	89.9	1664	3	US-09-582-224A-5	Sequence 5, Appli
4	1678.5	89.9	1664	3	US-09-023-655-1213	Sequence 1213, Ap
5	1678.5	89.9	1679	3	US-09-517-605-14	Sequence 14, Appl
6	1678.5	89.9	1737	2	US-08-202-056-4	Sequence 4, Appli
7	1678.5	89.9	1737	2	US-08-076-093A-3	Sequence 3, Appli
8	1678.5	89.9	1737	2	US-08-701-265-3	Sequence 3, Appli
9	1678.5	89.9	1737	2	US-08-284-586-3	Sequence 3, Appli
10	1678.5	89.9	1737	2	US-08-805-478-3	Sequence 3, Appl1
11	1678.5	89.9	1737	2	US-08-802-627A-3	Sequence 3, Appl1
12	1678.5	89.9	1737	2	US-08-801-238-3	Sequence 3, Appl1
13	1678.5	89.9	1737	2	US-08-801-228-3	Sequence 3, Appl1
14	1678.5	89.9	1737	6	US-09-104-296-3	Sequence 3, Appl1
15	1678.5	89.9	1059	6	PCT-US94-06380-2	Sequence 2, Appl1
16	1672.5	89.6	1317	3	US-09-826-509-484	Sequence 484, App
17	1672.5	89.6	1317	3	US-08-153-848-45	Sequence 45, Appl1
18	1672.5	89.6	1317	3	US-09-299-843A-45	Sequence 45, Appl1
19	1672.5	89.6	1317	6	US-09-088-337B-45	Sequence 45, Appl1
20	1672.5	89.6	1317	6	PCT-US93-11153-45	Sequence 45, Appl1
21	584	31.3	1107	3	US-09-170-496D-19	Sequence 19, Appl1
22	584	31.3	1293	3	US-09-016-434-1052	Sequence 1052, Ap
23	584	31.3	1670	3	US-08-709-838-1	Sequence 1, Appl1
24	584	31.3	1670	3	US-08-829-839-1	Sequence 1, Appl1
25	584	31.3	1670	3	US-09-023-655-980	Sequence 980, App
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28	580	31.1	1107	3	US-09-170-496D-173	Sequence 173, App
29	570.5	30.6	1607	3	US-08-875-573-19	Sequence 19, Appl1
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37	551.5	29.5	1200	6	PCT-US95-03032-1	Sequence 1, Appl1
38	550.5	29.5	1106	6	PCT-US92-02977-5	Sequence 5, Appl1
39	550.5	29.5	1106	6	PCT-US95-03032-4	Sequence 4, Appl1
40	550.5	29.5	2085	3	US-09-299-843A-65	Sequence 65, Appl1
41	550.5	29.5	2085	3	US-09-088-337B-65	Sequence 65, Appl1
42	546	29.2	440	3	US-09-513-999C-1915	Sequence 1915, Ap
43	544.5	29.2	1373	6	PCT-US92-02977-6	Sequence 6, Appl1
44	544.5	29.2	1373	6	PCT-US95-03032-3	Sequence 3, Appl1
45	544.5	29.2	1510	6	US-07-759-568-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-647-501-1
; Sequence 1, Application US/09647501
; Patent No. 6863887
; GENERAL INFORMATION:
; APPLICANT: No. 6863887thwest Biotherapeutics, Inc.
; APPLICANT: Murphy, Gerald P.
; APPLICANT: Boynton, Alton L.
; APPLICANT: Sehgal, Anil
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
; TITLE OF INVENTION: ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
; FILE REFERENCE: 20093-000600PC
; CURRENT APPLICATION NUMBER: US/09/647,501
; CURRENT FILING DATE: 2000-09-24
; PRIOR APPLICATION NUMBER: 60/079,916
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/104,656
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-647-501-1

Alignment Scores:
Pred. No.: $4.56e-189$ Length: 1059
Score: 1678.50   Matches: 319
Percent Similarity: 95.48%   Conservative: 19
Best Local Similarity: 90.11%   Mismatches: 11
Query Match: 89.90%   Indels: 5
DB: 3   Gaps: 1

Db   1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC 1056

RESULT 2
US-09-016-434-1235
; Sequence 1235, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
;   APPLICANT: Janice Au-Young
;   APPLICANT: Jeffrey J. Seilhamer
;   TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
;   TITLE OF INVENTION: PATHWAY GENE EXPRESSION
;   NUMBER OF SEQUENCES: 1490
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;   STREET: 3174 PORTER DRIVE
;   CITY: PALO ALTO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 94304
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/016,434
;   FILING DATE: HEREWITH
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Zeller, Karen J.
;   REGISTRATION NUMBER: 37,071
;   REFERENCE/DOCKET NUMBER: PA-0002 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650) 855-0555
;   TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1235:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1225 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
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;   CLONE: g189313
US-09-016-434-1235

Alignment Scores:
Pred. No.:   5.68e-189   Length: 1225
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Percent Similarity: 95.48%   Conservative: 19
Best Local Similarity: 90.11%   Mismatches: 11
Query Match: 89.90%   Indels: 5
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US-09-367-052-2 (1-359) x US-09-016-434-1235 (1-1225)

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Qy   126 ValLeuLeuLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
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 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: cDNA of CXCR4
US-09-582-224A-5

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Pred. No.:                                    Length:              1664
Score:                   9.01e-189            Matches:             319
Percent Similarity:      1678.50              Conservative:        19
Best Local Similarity:   95.48%               Mismatches:          11
Query Match:             90.11%               Indels:              5
DB:                      89.90%               Gaps:                1
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Qy     86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValHisAlaMetAlaAspTrpTyr 105
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Db    731 TATTGCATTATCATCTCACTCTCCCAAGGGCCACCAGAAGCGCAAGGCCCTC 790

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Qy    106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db    335 TTTGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT 394

Qy    126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db    395 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 454

Qy    146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
Db    455 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT 514

Qy    166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlyAspIleSer 185
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Db    515 GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAACGTC---------AGT 559

Qy    186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
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Db    560 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTTGTG 619

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Qy    246 LysThrThrValIleLeuLeuAlaPheLeuAlaCysTrpLeuProTyrTyrValGly 265
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Db    740 AAGACCACAGTCATCCTCATCCTGGCTTTCTTGGCCTGTTGGCTGCCTTACTACATTGGG 799

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Qy    306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
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RESULT 3
US-09-582-224A-5
 ; Sequence 5, Application US/09582224A
 ; Patent No. 6429308
 ; GENERAL INFORMATION:
 ; APPLICANT:  IIJIMA, Osamu
 ; APPLICANT:  GOTO, Takeshi
 ; APPLICANT:  SHIMADA, Takashi
 ; TITLE OF INVENTION: HIV Infection Inhibitors
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/582,224A
 ; CURRENT FILING DATE:  2000-07-21
 ; PRIOR APPLICATION NUMBER: PCT/JP99/06534
 ; PRIOR FILING DATE: 1999/11/24
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Query Match:        89.90%   Indels:   5
DB:                 3        Gaps:     1

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Db   206 ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGCTCATG   265

Qy    66 GlyTyrGlnLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla     85
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   266 GGTTACCAGAAGAAACTGAGAAGCATGACCGACAAGTACAGGCTGCACCTGTCAGTGGCC   325

Qy    86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr   105
          ::::||||||||||||||||||||||||||||::::||||||||:::::||||::
Db   326 GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTGGATGCGATGGCAAACTGGTAC   385

Qy   106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer   125
          :::||||||||||||||||||||||||||||| ::||||||||||||||||||||||||
Db   386 TTTGGAACTTCCTATGCAAGGCAGTCCATGTCATCATCACACAGTCAACCTCTACAGCAGT   445

Qy   126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn   145
          ::::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   446 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC   505

Qy   146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro   165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   506 AGTCAGAGGCCAAGGAAGCTGTTGGCAGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT   565

Qy   166 AlaLeuLeuLeuThrIleProAspProPheIlePheAlaSerGlnGlyAspIleSer     185
          ||||||||||||||||||||||||||||||||||::
Db   566 GCCCTCCTGCTGACTATTCCCGACTCATCTTGCCAACGTC--------AGT          610

Qy   186 GlnGlyAspAspArgTyrIleCysAspArgLeuTrpProAspSerLeuTrpMetValVal   205
          :::  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   611 GAGGCAGATGACAGATATCTGTGACCGGCTTCTACCCCAATGACTTGTGGGTGGTGTG     670

Qy   206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys   225
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   671 TTCCAGTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC   730

Qy   226 TyrCysIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu     245
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   731 TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC   790

Qy   246 LysThrThrValIleLeuLeuLeuLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly   265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||::::
Db   791 AAGACCACAGTCATCCTGCTTTCTTCCGCCTGTTGGCTGCCTTACTACATTGGG        850

Qy   266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnCysAspAsnPheGluSer   285
          |||||||||||||||||||||||||||||||  ::||||||||||||||||||||||||
Db   851 ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAGTGTGAGTTTGAGAAC     910

Qy   286 IleValHisTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn     305
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   911 ACTGTGCACAGTGGATTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC   970

Qy   306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn   325
          :::||||||||||||||||||||||||||||||::::||||||||||||||||||||||
Db   971 CCCATCCTCTACGCTTTCCTGGAGCAAAATTAAAACCTCTGCCCAGCACGCACTCACC  1030

Qy   326 SerMetSerArgGlySerSerLeuLysLeuSerLeuLysLeuGlyArgGlyValHisSer   345
          |||||||||||||||||||||||||||||||||||||||||||||::||
Db  1031 TCTGTGAGCAGAGGGTCCAGCCTCCAAGATCCTCTTCCCAAAGAAAGGGAGGTGGACATTCA  1090
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Db   851 ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAGTGTGAGTTTGAGAAC   910
          :::||||||||||
Qy   286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn   305

Db   911 ACTGTGCACAGTGGATTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC   970
          |||||||||||||||
Qy   306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn   325

Db   971 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCACGACCACTCACC  1030
          :::||||||||||||||||::
Qy   326 SerMetSerArgGlySerSerLeuLysIleLeuLeuSerLeuSerLeuArgGlyHisSer   345

Db  1031 TCTGTGAGCAGAGGGTCCAGCCTCCAGATCCTCTTCCTGGAGCCACACCTGTGGACATTCA  1090
          ||||||||||||||||||||
Qy   346 SerValSerThrGluSerGluSerPheHisSerSer  359
          ||||||||||||||||||||||||||||||||||||
Db  1091 TCTGTTTCCACTGAGTCTGAGTCTTTCCACTCCAGC  1132
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RESULT 4

US-09-023-655-1213

; Sequence 1213, Application US/09023655
; Patent No. 6607879
GENERAL INFORMATION:
  APPLICANT: Cocks, Benjamin G.
  APPLICANT: Seilhamer, Susan G.
  APPLICANT: Seilhamer, Jeffrey J.
  TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
  TITLE OF INVENTION: EXPRESSION
  NUMBER OF SEQUENCES: 1508
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
    STREET: 3174 PORTER DRIVE
    CITY: PALO ALTO
    STATE: CALIFORNIA
    COUNTRY: USA
    ZIP: 94304
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/023,655
    FILING DATE: HEREWITH
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER:
    FILING DATE:
  CLASSIFICATION:
  ATTORNEY/AGENT INFORMATION:
    NAME: Zeller, Karen J.
    REGISTRATION NUMBER: 37,071
    REFERENCE/DOCKET NUMBER: PA-0001 US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (650) 855-0555
    TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1213:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1664 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
  IMMEDIATE SOURCE:
    LIBRARY: GENBANK
    CLONE: 9219868
US-09-367-052-2-1213

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Alignment Scores:
Pred. No.:              9.01e-189       Length:          1664
Score:                  1678.50         Matches:          319
Percent Similarity:     95.48%          Conservative:      19
Best Local Similarity:  90.11%          Mismatches:        11
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Qy    346 SerValSerThrGluSerSerPheHisSerSer 359
Db   1091 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC 1132

RESULT 5
US-09-517-605-14
; Sequence 14, Application US/0951605
; Patent No. 6391567
; GENERAL INFORMATION:
;   APPLICANT: Littman, Dan R.
;   APPLICANT: Kwon, Douglas S.
;   APPLICANT: van Kooyk, Yvette
;   APPLICANT: Geijtenbeck, Theo
;   TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
;   TITLE OF INVENTION: CELLS
;   FILE REFERENCE: 1049-1-017
;   CURRENT APPLICATION NUMBER: US/09/517,605
;   CURRENT FILING DATE: 2000-03-02
;   NUMBER OF SEQ ID NOS: 17
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 1679
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-517-605-14

Alignment Scores:
Pred. No.:               9.13e-189      Length:        1679
Score:                   1678.50        Matches:       319
Percent Similarity:      95.48%         Conservative:  19
Best Local Similarity:   90.11%         Mismatches:    11
Query Match:             89.90%         Indels:        5
DB:                                     Gaps:          1

US-09-367-052-2 (1-359) x US-09-517-605-14 (1-1679)

Qy      6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
            ::|||||||||||||||||:|:::::|||||::|||::||:||||||||||||||||
Db     98 ATCAGTATATACACTTCAGATAACTACACACCGAGGAAATGGGCTCAGGGGACTATGACTCC 157

Qy     26 AsnLysGluProCysPheArgAspLeuAsnValHisPheAsnArgIlePheLeuProThr 45
            ||||||:||::||||||||||     ::|||||||:||||||||||:||||||
Db    158 ATGAAGGAACCCTGTTTCCGTGAAGAAATATGCTAATTCAATAAAATCTTCCTGCCCACC 217

Qy     46 IleTyrPheIleIlePheLeuPheGlyIleValGlyTyrIleValGlyAsnValIleLeuValMet 65
            |||::||||:||||||||||||||||||||||||||||||||||||||||||
Db    218 ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 277

Qy     66 GlyTyrGlnLysLeuArgSerMetThrArgLysTyrArgLeuHisLeuSerValAla 85
            ||||:||||||||||||:||||||||||||||||||||||||||||||:||||
Db    278 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC 337

Qy     86 AspLeuLeuPheValIleThrLeuProPhePheTrpAlaValAspAlaMetAlaAspTrpTyr 105
            |||||||||||||||||||:||||||||||||||||||||||||||||||
Db    338 GACCTCCTCTTTGTCATCACGCTTCCCTTCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC 397

Qy    106 PheGlyLysPheLeuCysLysLysValAlaValAspIleTyrThrValAsnLeuTyrSerSer 125
            ||||||||||||::|||||||||||||||||||||||||||:||||||||
Db    398 TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTGAACCTCTACAGCAGT 457

Qy    126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    458 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 517

Qy    146 SerGlnArgProArgLysLeuLeuAlaGluLysArgValTyrValGlyValAlaValTrpIlePro 165
            |||:|||||||||||||||||||||||||||:|||||||||||||||||||
Db    518 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGAGGGTGTATGTTGGCGTCGCTGGATCCCT 577

Qy    166 AlaLeuLeuThrIleProArgAspPhePheProAlaAspValSerGlnGlyAspIleSer 185
            |||||||||||||||||::::::|||||||||::|||       ---------AGT
Db    578 GCCCTCCTGCTGCTACATTCCCGGACTATCTTTTGCCAACGTC---------AGT 622

Qy    186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
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Db    623 GAGGCAGATGACAGATATCTGTGACCCGCTTCACCCCAATGACTTGTGGGTGGTTGTG 682
            ::: |||||||||||||||||||||||||    |||||:::  |||||||||||

Qy    206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleLeuIleLeuSerCys 225
            |||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db    683 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGTATTGTCATCCTGTCCTGC 742

Qy    226 TyrCysIleIleIleSerLysSerLeuSerHisSerLysSerHisGlnLysArgLysAlaLeu 245
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    743 TATTGCATTATCATCTCCAAGTCTCACACTCCAAGGGCCACCAGAAGCCAAGGCCCTC 802

Qy    246 LysThrThrValIleLeuLeuLeuAlaPhePheAlaCysTrpLeuProTyrTyrLeuGlyLeuValGly 265
            |||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db    803 AAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGCTGCCTTACTACATTGGG 862

Qy    266 IleSerIleAspSerPheIleLeuLeuGlyValIleLeuLysGlnLysCysAspPheGluSer 285
            ||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db    863 ATCAGCATCGACTCCTTCATCCTCCTGGGAAATCATCAAGCAAGGGGTGAGTTTGAGAAC 922

Qy    286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
            ||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db    923 ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC 982

Qy    306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
            ||||||||||||||||||||||||||:|||||||||||||||:|||||||||||||
Db    983 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC 1042

Qy    326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysLysArgGlyGlyHisSer 345
            ||:::||||||||||||||||||||||||||||||||||||||||||||
Db   1043 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAGAAGAGCGAGGTGGACATTCA 1102

Qy    346 SerValSerThrGluSerSerPheHisSerSer 359
            ||||||||||||||||||||||||||||||||||
Db   1103 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC 1144

RESULT 6
US-08-202-056-4
; Sequence 4, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
;   APPLICANT: Chuntharapai, Anan
;   APPLICANT: Hebert, Caroline
;   APPLICANT: Kim, Kyung Jin
;   APPLICANT: Lee, James
;   TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genentech, Inc.
;     STREET: 460 Point San Bruno Blvd
;     CITY: South San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: patin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/202,056
;     FILING DATE: 25-FEB-1994
;     CLASSIFICATION: 436
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/677211
;     FILING DATE: 29-MAR-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Love, Richard B.
;     REGISTRATION NUMBER: 34,659
;     REFERENCE/DOCKET NUMBER: 706P3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415/225-5530
;     TELEFAX: 415/952-9881
;     TELEX: 910/371-7168
```

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;   INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1737 bases
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
US-08-202-056-4

Alignment Scores:
Pred. No.:              9.61e-189
Score:                  1678.50
Percent Similarity:     95.48%
Best Local Similarity:  90.11%
Query Match:            5
DB:                     1

US-09-367-052-2 (1-359) x US-08-202-056-4 (1-1737)

Qy     6  ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyTyrAspTyr   25
          ::|||||||||||||||||||||||||:||||:|||:|||||
Db   100  ATCAGTATATACACTTCAGATAACTAACACCGAGGAAATGGGCTTCAGGGGACTATGACTCC  159

Qy    26  AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr   45
          ||||||||||::||||||||||||||||::|:||||||
Db   160  ATGAAGGAACCCCTGTTCCGTGACGAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC  219

Qy    46  IleTyrPheIleIlePheLeuThrGlyTyrIleValGlyLeuValIleLeuValMet   65
          ||||||||||||||||||||||||
Db   220  ATCTACTTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGAATTGGTCATCCTGGTCATG  279

Qy    66  GlyTyrGlnLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla   85
          |||||||||||||||||||||||||||||
Db   280  GGTTACCAGAAGAAACTGAGAAGCATGACGACGAAGTACAGGCTGCACCTGTCAGTGGCC  339

Qy    86  AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr  105
          ::|:|||||||||||
Db   340  GACCTCCTTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGCAAACTGGTAC  399

Qy   106  PheGlyLysPheLeuCysLysValAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
          |||||           ||||||||
Db   400  TTTGGGAACTTCCTATGCAAGGAGTCCATGTCATCACACAGTCAACCTCACAGCAGT  459

Qy   126  ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
          |||||||||||||||||||||||||||
Db   460  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC  519

Qy   146  SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro  165
          ||||||||||||||||||||||||
Db   520  AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT  579

Qy   166  AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer  185
          ||||||||||||||||||||
Db   580  GCCCTCCTGCTGCTAATTCCCGACTTCATCTTTGCCAACGTC----------AGT  624

Qy   186  GlnGlyAspAspAsnArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal  205
          :::           |||||||
Db   625  GAGGCAGATGACAGATATATCTGTGACCGCCTTCTACCCCAATGACTTGTGGGTGGTTGTG  684

Qy   206  PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys  225
          |||||||
Db   685  TTCCAGTTTCAGCACATCATGGTGGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC  744

Qy   226  TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu  245
          |||||||
Db   745  TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC  804

Qy   246  LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly  265
          |||||           :::|||
Db   805  AAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGCTGCCTTACTACATTGGG  864

Qy   266  IleSerIleAspPhePheIleLeuLeuGluIleValLysGlnGlyCysAspPheGluSer  285
          |||||           ::|||
Db   865  ATCAGCATCGACTTCTTCATCCTCCTGGAAATCATCAAGCAAGGTGTGAGTTTGAGAAC  924
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Qy   286  IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn  305
          ||||||||||||
Db   925  ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTGTCTGAAC  984

Qy   306  ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn  325
          ||||||||
Db   985  CCCATCCTCTATGCTTTCCTTGGAGCCAAATTAAAACCTTGCCCAGCACACGCACTCACC  1044

Qy   326  SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer  345
          ||::|||||||||
Db  1045  TCTGTGAGCAGAGAGGGTCCAGCCTCCAAGATCCTCTCCAAGGAAAGCGAGTGGACATTCA  1104

Qy   346  SerValSerThrGluSerGluSerSerPheHisSerSer  359
          |||||
Db  1105  TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCCAGC  1146
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```
RESULT 7
US-08-076-093A-3
;  Sequence 3, Application US/08076093A
;  Patent No. 5543503
;  GENERAL INFORMATION:
;    APPLICANT: Chuntharapai, Anan
;    APPLICANT: Lee, James
;    APPLICANT: Hebert, Caroline
;    APPLICANT: Jin Kim, K.
;    TITLE OF INVENTION: Antibodies to Human PF4A Receptors
;    NUMBER OF SEQUENCES: 6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Genentech, Inc.
;      STREET: 460 Point San Bruno Blvd
;      CITY: South San Francisco
;      STATE: California
;      COUNTRY: USA
;      ZIP: 94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/076,093A
;      FILING DATE: 11-Jun-1993
;      CLASSIFICATION: 530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 07/810782
;      FILING DATE: 19-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 07/677211
;      FILING DATE: 29-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Love, Richard B
;      REGISTRATION NUMBER: 34,659
;      REFERENCE/DOCKET NUMBER: 706P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 415/225-5530
;      TELEFAX: 415/952-9881
;      TELEX: 910/371-7168
;    INFORMATION FOR SEQ ID NO: 3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 1737 nucleotides
;      TYPE: Nucleic Acid
;      STRANDEDNESS: Single
;      TOPOLOGY: Linear
US-08-076-093A-3

Alignment Scores:
Pred. No.:              9.61e-189
Score:                  1678.50
Percent Similarity:     95.48%
Best Local Similarity:  90.11%
Query Match:            2
DB:
```

```
Length:        1737
Matches:       319
Conservative:  19
Mismatches:    11
Indels:        5
Gaps:          1
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Length:        1737
Matches:       319
Conservative:  19
Mismatches:    11
Indels:        5
Gaps:          1
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Db   1105 TCTGTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC 1146

RESULT 8
US-08-701-265-3
; Sequence 3, Application US/08701265
; Patent No. 5776457
; GENERAL INFORMATION:
;   APPLICANT: Chuntharapai, Anan
;   APPLICANT: Lee, James
;   APPLICANT: Hebert, Caroline
;   APPLICANT: Jin Kim, K.
;   TITLE OF INVENTION: Antibodies to Human PF4A Receptors
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 460 Point San Bruno Blvd
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/701,265
;   FILING DATE: 22-AUG-1996
;   CLASSIFICATION: 424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/076093
;   FILING DATE: 11-Jun-1993
;   APPLICATION NUMBER: 07/810782
;   FILING DATE: 19-DEC-1991
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/677211
;   FILING DATE: 29-MAR-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Love, Richard B
;   REGISTRATION NUMBER: 34,659
;   REFERENCE/DOCKET NUMBER: 706P2
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415/225-5530
;   TELEFAX: 415/952-9881
;   TELEX: 910/371-7168
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1737 nucleotides
;   TYPE: Nucleic Acid
;   STRANDEDNESS: Single
;   TOPOLOGY: Linear
;
US-08-701-265-3

Alignment Scores:
Pred. No.:   9.61e-189   Length: 1737
Score: 1678.50   Matches: 319
Percent Similarity: 95.48%   Conservative: 19
Best Local Similarity: 90.11%   Mismatches: 11
Query Match: 89.90%   Indels: 5
DB: 2   Gaps: 1

US-09-367-052-2 (1-359) x US-08-701-265-3 (1-1737)

Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyTyrAspSer 25
            :::|||||||||||||||||||||||||||::::|||||
Db   100 ATCAGTATATACACTTCAGATAACTACACCGGAGAAATGGGCTCAGGGACTATGACTCC 159

Qy   26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
            |||||||||||:||:|||||||||||||||||||||||||:|||
Db   160 ATGAAGGAACCCTGTTTCCGTGAAGAAATGCTAATTTCAATAAAATCTTCCTGCCCACC 219

Qy   46 IleTyrPheIleIlePheLeuThrGlyTyrIleValGlyAsnGlyLeuValIleLeuValMet 65
            ||||||
Db   220 ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 279

Qy   66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
            ||||||
Db   280 GGTTACCAGAAGAAACTGAGAAGCATGACCGACAAGTACAGGCTGCACCTGTCAGTGGCC 339

Qy   86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
            ||||||
Db   340 GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCATGGCAGACTGGTAC 399

Qy   106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
            |||||||||||||
Db   400 TTTGGAAACTTCCTATGCAAGGCAGTCCATATCATCTACACAGTCAACCTCTACAGCAGT 459

Qy   126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
            |||||||||||||||||
Db   460 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 519

Qy   146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
            |||||||
Db   520 AGTCAGAGGCCCAGGAAGCTGTTGGCTGAAAAGGCTGTCTATGTTGGCGTCTGGATCCCT 579

Qy   166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
            ||||
Db   580 GCCCTCCTGCTGACTATCCCGACTTCATCTTTGCCAAGTC----------AGT 624

Qy   186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
            :::||:||||||:|||||
Db   625 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGATGGTTGTG 684

Qy   206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
            ||||||||||||
Db   685 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC 744

Qy   226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
            |||||
Db   745 TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 804

Qy   246 LysThrThrValIleLeuIleLeuAlaPheAlaCysTrpLeuProTyrTyrValGlyGly 265
            :::|||
Db   805 AAGACCACAGTCATCCTCATCCTCGCCTTTGCTTGCTGGCTCCCTTACTACATTGGG 864

Qy   266 IleSerIleAspSerPheIleLeuLeuGlyIleIleLysGlnGlyCysAspPheGluSer 285
            :::|||||||||||||
Db   865 ATCAGCATCGACTCCTTCATCCTCCTGGGAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 924

Qy   286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsn 305
            |||||||||||
Db   925 ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTTCTTCCACTGTTGTCTGAAC 984

Qy   306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerArgAlaGlnHisAlaLeuAsn 325
            :::|||||||||||||
Db   985 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTCGCCAGCACACCACT 1044

Qy   326 SerMetSerArgGlySerLeuLysLeuIleLeuSerLysGlyGlyArgGlyHisSer 345
            |||||||||||||
Db   1045 TCTGTGAGCAGAGGTCCAGGGTCTCAAGATCCTCCAAGATCCTCCAAAGGAAAGCGAGGTGGACATTCA 1104

Qy   346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
            ||||||

```
CORRESPONDENCE ADDRESS:
  ADDRESSEE:  Genentech, Inc.
  STREET:  460 Point San Bruno Blvd
  CITY:  South San Francisco
  STATE:  California
  COUNTRY:  USA
  ZIP:  94080
COMPUTER READABLE FORM:
  MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
  COMPUTER:  IBM PC compatible
  OPERATING SYSTEM:  PC-DOS/MS-DOS
  SOFTWARE:  WinPatin (Genentech)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER:  US/08/284,586
  FILING DATE:
  CLASSIFICATION:  424
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:  US/08/076,093A
  FILING DATE:  11-Jun-1993
  APPLICATION NUMBER:  07/810782
  FILING DATE:  19-DEC-1991
PRIOR APPLICATION DATA:
  APPLICATION NUMBER:  07/677211
  FILING DATE:  29-MAR-1991
ATTORNEY/AGENT INFORMATION:
  NAME:  Love, Richard B
  REGISTRATION NUMBER:  34,659
  REFERENCE/DOCKET NUMBER:  706P2
TELECOMMUNICATION INFORMATION:
  TELEPHONE:  415/225-5530
  TELEFAX:  415/952-9881
  TELEX:  910/371-7168
INFORMATION FOR SEQ ID NO:  3:
  SEQUENCE CHARACTERISTICS:
  LENGTH:  1737 nucleotides
  TYPE:  Nucleic Acid
  STRANDEDNESS:  Single
  TOPOLOGY:  Linear
US-08-284-586-3
```

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Alignment Scores:
Pred. No.:                                Length:           1737
Score:                    9.61e-189       Matches:           319
Percent Similarity:       1678.50         Conservative:       19
Best Local Similarity:    95.48%          Mismatches:         11
Query Match:              90.11%          Indels:              5
DB:                       89.90%          Gaps:                1
                          2
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US-09-367-052-2 (1-359) x US-08-284-586-3 (1-1737)

```
Qy    6  ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer              25
         :::||||||:|||:::|||||||||||||:||||||||||||||||||||||||:||
Db  100  ATCAGTATATACACTTCAGATAACTACACCGAGAAAATGGCTGAGACAAGTACAGGCTGCACCTGTCAGTGGCC  159

Qy   26  AsnLysGluProCysPheArgAspAspGluAsnValHisIleTrpLeuAsnAlaHisArgIlePheLeuProThr  45
         ||||:|||||:||||:|||::|||||||:|:|||||:||::||||||||||:::||||||||||||||||||||
Db  160  ATGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC                 219

Qy   46  IleTyrPheIleIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet               65
         |||||||:|||:::|||:|||::|:|||||||:||:||||||||:||||||||:|||||||
Db  220  ATCTACTCCATCATCTTCTTAACTGGCAATGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG            279

Qy   66  GlyTyrGlnLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla                     85
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  280  GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC                  339

Qy   86  AspLeuMetPheValIleThrLeuProPheThrLeuAlaValAspAlaMetAlaAspTrpTyr              105
         |||||||||||||||||||||||||||||||:|:||:||||||||:::|||||||||||||
Db  340  GACCTCCTTTGTCATCACGCGTTCCCTTCGGGCAGTTGATGCCGTGGCAAACTGGTAC                   399

Qy  106  PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer                 125
         ||||||||||:|||||||||||||||||||:|||:||||||||||||||||||:|||||
Db  400  TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT                  459

Qy  126  ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn                 145
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  460  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC                  519

Qy  146  SerGlnArgProArgLysLeuAlaGluLysArgValThrValGlyValTrpIlePro                    165
         ||||||:||||||:||||||||||||||||||:|||||||||||||||||||||||||
Db  520  AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGCGTGTCACTGTTGGGGTCTGGATCCCT                  579

Qy  166  AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer                 185
         |||||||||||||||||||||||||||||||||||||||:::|:::||||
Db  580  GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAACGTC------------AGT                    624

Qy  186  GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal                 205
         :::    :|||:||||||||||||||||||||||:|||||||||||||||||||||||
Db  625  GAGGCAGATGACAGATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTTGTG                    684

Qy  206  PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValLeuLeuSerCys                 225
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  685  TTCCAGTTTCAGCACATCATGGTTGGCCTTATTCTGCCTGGTATTGTCATCCTGTCCTGC                  744

Qy  226  TyrCysIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu                    245
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  745  TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC                  804

Qy  246  LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly                 265
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db  805  AAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGCTGCCTTACTACATTGGG                  864

Qy  266  IleSerIleAspAspPheLeuLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer                 285
         ||||||:||||||  :::|||||||||||:|||  ||:||||||||:|||||||||||
Db  865  ATCAGCATCGACTTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC                 924

Qy  286  IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn                 305
         ||::||:|||||||||||:|||||||||||||||||||||||||||||||||||||||
Db  925  ACTGTGACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC                   984

Qy  306  ProIleLeuTyrAlaPheLeuGlyLeuAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn              325
         ||||||||||||||||||||||||:|||||||:||||||||||||:|:||||||||||||
Db  985  CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCCACTCACC                 1044

Qy  326  SerMetSerArgGlySerGlnArgLeuIleLeuSerLysLysGlyGlyHisGlnSer                    345
         |||:::|||||||||:||||||||||||||||||||||||||||||||:::||||||
Db 1045  TCTGTGACCAGAGGGTCCCAGCGTCTCATCCTCAAGAAGGAAGCGAGGTGACATTCA                     1104

Qy  346  SerValSerThrGluSerGluSerSerSerPheHisSerSer                                   359
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Db 1105  TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC                                    1146
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RESULT 9
US-08-284-586-3
; Sequence 3, Application US/08284586
; Patent No. 5840856
; GENERAL INFORMATION:
;   APPLICANT: Chuntharapai, Anan
;   APPLICANT: Lee, James
;   APPLICANT: Hebert, Caroline
;   APPLICANT: Jin Kim, K.
;   TITLE OF INVENTION: Antibodies to Human PF4A Receptors
;   NUMBER OF SEQUENCES: 6
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APPLICATION NUMBER:  US/08/805,478
FILING DATE:  25-Feb-1997
CLASSIFICATION:  530
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  08/284586
    FILING DATE:  10-AUG-1994
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  08/076093
    FILING DATE:  11-JUN-1993
PRIOR APPLICATION DATA:
    APPLICATION NUMBER:  07/810782
    FILING DATE:  19-DEC-1991
ATTORNEY/AGENT INFORMATION:
    NAME:  Love, Richard B.
    REGISTRATION NUMBER:  34,659
    REFERENCE/DOCKET NUMBER:  P0706P2P1C1
TELECOMMUNICATION INFORMATION:
    TELEPHONE:  415/225-5530
    TELEFAX:  415/952-9881
    TELEX:  910/371-7168
INFORMATION FOR SEQ ID NO:  3:
    SEQUENCE CHARACTERISTICS:
    LENGTH:  1737 base pairs
    TYPE:  Nucleic Acid
    STRANDEDNESS:  Single
    TOPOLOGY:  Linear
US-08-805-478-3
```

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Alignment Scores:
Pred. No.:                                    Length:        1737
Score:                     9.61e-189          Matches:        319
Percent Similarity:        1678.50            Conservative:    19
Best Local Similarity:     95.48%             Mismatches:      11
Query Match:               90.11%             Indels:           5
DB:                        89.90%             Gaps:             1
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US-09-367-052-2 (1-359) x US-08-805-478-3 (1-1737)

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Qy    6  ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer   25
Db  100  ATCAGTATATACACTTCAGATAACTAACACCGAGGAAATGGGCTCAGGGGACTATGACTCC  159

Qy   26  AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr   45
Db  160  ATGAAGGAACCCTGTTTCCGTGAAGAAAATGTCATTTCAATAAAATCTTCTGCCCACC    219

Qy   46  IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet   65
Db  220  ATCTACTTCATCATCTTTCTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG  279

Qy   66  GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla   85
Db  280  GGTTACCAGAAGAAACTGAGAAGCATGACAGACAAGTACAGACTCCACCTGTCAGTGGCC  339

Qy   86  AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr  105
Db  340  GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC  399

Qy  106  PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
Db  400  TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACTTCTACAGCAGT  459

Qy  126  ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
Db  460  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC  519

Qy  146  SerGlnArgProArgLysLeuLeuAlaGluLysValValTyrValGlyValTrpIlePro  165
Db  520  AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT  579

Qy  166  AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer  185
Db  580  GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAAGTC--------------AGT  624
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Qy  126  ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
Db  460  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGGTACCTGGCCATCGTCCACGCCACCAAC  519

Qy  146  SerGlnArgProArgLeuGluLeuAlaGluLysAlaValTyrValGlyValTrpIlePro  165
Db  520  AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT  579

Qy  166  AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer     185
Db  580  GCCCTCCTGCTGACATTCCCGACTTCATCTTTGCCAAGTC----------AGT        624

Qy  186  GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal  205
Db  625  GAGGCAGATGACAGATATCTGTGACCGGCTTCTACCCCAATGACTTGTGGGTGGTTGTG   684

Qy  206  PheGlnPheGlnHisHisMetValGlyLeuLeuProGlyTyrIleValIleLeuSerCys  225
Db  685  TTCCAGTTTCAGCAACATCATGGTTGGCCTATCCTGCCTGGTATTGTCATCCTGTCCTGC  744

Qy  226  TyrCysIleIleSerIleLeuSerGlyHisIleGlnArgLysArgLysAlaLeu       245
Db  745  TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAGGCGAAGGCCCTC   804

Qy  246  LysThrThrValIleLeuLeuLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly  265
Db  805  AAGACCACAGTCATCCTCACTCCTGGCTTTCTTGCCTGTTGGCTGCCTACTACATTGGG   864

Qy  266  IleSerIleAspSerPheIleLeuLeuGlyIleLysGlnGlyCysAspAspPheGluSer  285
Db  865  ATCAGCATCGACTCCTTCATCCTCCTGGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 924

Qy  286  IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsn     305
Db  925  ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC  984

Qy  306  ProIleLeuTyrAlaPheLeuGlyAlaLysPheSerSerAlaGlnHisAlaLeuAsn     325
Db  985  CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC 1044

Qy  326  SerMetSerArgGlySerPheLeuLeuSerLeuLysSerTyrLysGlyArgGlyHisSer  345
Db 1045  TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA 1104

Qy  346  SerValSerThrGluSerGlySerSerPheHisSerSer                      359
Db 1105  TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC                   1146
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RESULT 10
US-08-805-478-3
; Sequence 3, Application US/08805478
; Patent No. 5874543
; GENERAL INFORMATION:
;   APPLICANT:  Chuntharapai, Anan
;   APPLICANT:  Lee, James
;   APPLICANT:  Hebert, Caroline
;   APPLICANT:  Jin Kim, K.
;   TITLE OF INVENTION:  ANTIBODIES TO PF4A RECEPTOR
;   NUMBER OF SEQUENCES:  6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genentech, Inc.
;     STREET:  460 Point San Bruno Blvd
;     CITY:  South San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
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```
;       REGISTRATION NUMBER: 34,659
;       REFERENCE/DOCKET NUMBER: P0706P2P1D2
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: 415/225-5530
;          TELEFAX: 415/952-9881
;          TELEX: 910/371-7168
;  INFORMATION FOR SEQ ID NO: 3:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 1737 base pairs
;        TYPE: Nucleic Acid
;        STRANDEDNESS: Single
;        TOPOLOGY: Linear
; US-08-802-627A-3

Alignment Scores:
Pred. No.:                              Length:                1737
Score:                     9.61e-189    Matches:               319
Percent Similarity:        1678.50      Conservative:          19
Best Local Similarity:     95.48%       Mismatches:            11
Query Match:               90.11%       Indels:                5
DB:                        89.90%       Gaps:                  1
                           2

US-09-367-052-2 (1-359)  x  US-08-802-627A-3  (1-1737)
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Qy      6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
            :::||||||||||||||||||||||||||||||||| :::|||||||||||||||
Db    100 ATCAGTATATACACTTCAGATAACTACACCAGGGAAATGGCTCAGGGACTATGACTCC 159

Qy     26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
            |||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db    160 ATGAGAGGAACCCTGTTTCCCTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC 219

Qy     46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 ATCTACTTCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 279

Qy     66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC 339

Qy     86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
            ||||||||||||||||||||||||||||||||||||||||||||::|||||||||
Db    340 GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC 399

Qy    106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
            |||||||||||||:::|||||||||||||||||||::|||||||:::||||||||||
Db    400 TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT 459

Qy    126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 519

Qy    146 SerGlnArgProArgLysLeuLeuAlaGluLysValValTyrValGlyValTrpIlePro 165
            |||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db    520 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT 579

Qy    166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnAspIleIleSer 185
            |||||||||||||||||||||||||||||||||||||||:::|||
Db    580 GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAACGTC-------AGT 624

Qy    186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
            :::||||||||||||||||||||||||||||||||||||||||||||
Db    625 GAGGGCAGATGACAGATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTTGTG 684

Qy    206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC 744

Qy    226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 TATTGCATTATAATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 804

Qy    246 LysThrThrValIleLeuIleLeuAlaPheAlaCysTrpLeuProTyrTyrValGly 265
```

```
Qy    186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
            ::: |||||||||||||||||||||||||||||||||:::|||||||||
Db    625 GAGGGCAGATGACAGATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTTGTG 684

Qy    206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC 744

Qy    226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 TATTGCATTATAATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 804

Qy    246 LysThrThrValIleLeuIleLeuAlaPheAlaCysTrpLeuProTyrTyrValGly 265
            |||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db    805 AAGACCACAGTCATCCTCATCCTGGCTTTCGCCTGTTGGCTGCCTTACTACATTGGG 864

Qy    266 IleSerIleAspSerPheIleLeuLeuGlyIleIleLysGlnGlyCysAspPheGluSer 285
            |||||||||||||||||| :::||||||||||||||||||||||||||||||||
Db    865 ATCAGCATCGACTCCTTCATCCTCCTGGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 924

Qy    286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    925 ACTGTGCACAAGTGGATTTCCATCACCACGAGGCCCTAGCTTTCTTCCACTGTGTCTGAAC 984

Qy    306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
            |||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db    985 CCCATACTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC 1044

Qy    326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyGlyHisSerSer 345
            |||||||||||||||||||||||||||||||||||||||||||||
Db   1045 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGGGAGGTGGACATTCA 1104

Qy    346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
            |||||||||||||||||||||||||||||||||
Db   1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC 1146
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RESULT 11
US-08-802-627A-3
; Sequence 3, Application US/08802627A
; Patent No. 5892017
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 460 Point San Bruno Blvd
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/802,627A
;   FILING DATE: 19-Feb-1997
;   CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/284586
;   FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/076093
;   FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 07/810782
;   FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
;   NAME: Love, Richard B.
```

```
Alignment Scores:
Pred. No.:              9.61e-189          Length:         1737
Score:                  1678.50            Matches:         319
Percent Similarity:     95.48%             Conservative:     19
Best Local Similarity:  90.11%             Mismatches:       11
Query Match:            89.90%             Indels:            5
                                           Gaps:              1

US-09-367-052-2 (1-359)  x  US-08-801-238-3 (1-1737)

Qy      6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer  25
            :::||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
Db    100 ATCAGTATATACACTTCAGATAACTACACCAGGGAAATGGCTCAGGGGACTATGACTCC 159

Qy     26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr  45
            :::||||||||||||||||||||||::::|||||::::|||||||||||||||||||||
Db    160 ATGAAGGAACCCGTTTCCGTGAAGAAAAATGCTAATTTCATAAAATCTTCCTGCCCACC 219

Qy     46 IleTyrPheIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet  65
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    220 ATCTACTTCCATCATCTTCTTAACTGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 279

Qy     66 GlyTyrGlnLysLysLeuArgSerMetThrAspTyrTyrArgLeuHisLeuSerValAla  85
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    280 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAGTACAGGCTGCACCTGTCAGTGGCC 339

Qy     86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
            |||||||||||||||||||||||||||||||||||||||||||||::::|||||||||
Db    340 GACCTCCTTTTGTCATCACGTTCCCTTCCGTGGCAGTTGATGCCGTGGCAAACTGGTAC 399

Qy    106 PheGlyLysPheLeuCysLysValAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
            ||||||||||||||||||||||||||||||::::|||||||::::||||||||||||||||
Db    400 TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCACACAGTCAACCTCTACACGAGT 459

Qy    126 ValIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    460 GTCCCCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 519

Qy    146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    520 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT 579

Qy    166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnAspAspIleSer 185
            |||||||||||||||||||||||||||||||||||||||||||||||--------AGT 624
Db    580 GCCCTCCTGCTGACTATCCCGACTTCATCTTTGCCAACGTC--------------AGT 624

Qy    186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
            ::  |||||||||||||||||||||||||||||||| ||||||||::::||||||||||
Db    625 GAGGGCAGATGACAGATATATCTGTGACCGGCTTTACCCCAATGACTTGTGGGTGGTTGTG 684

Qy    206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    685 TTCCAGTTCCAGCACATCATGGTTGGCCTGATTGTCATCCTGCCTGGTATTGTCATCCTCTGCC 744

Qy    226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    745 TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 804

Qy    246 LysThrThrValIleLeuLeuLeuAlaPheTrpLeuProTyrTyrValGly 265
            ||||||||||||||||||||||||||||||||||||||||||::::|||
Db    805 AAGACCACAGTCATCCTCATCCTGGCTTTCTGGCTGCCTTACTACATTGGG 864

Qy    266 IleSerIleAspSerPheIleLeuLeuGluIleValIleLysGlyCysAspPheGluSer 285
            |||||||||||||||||||||||||||::::||||||||::::|||||||||||||||
Db    865 ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 924

Qy    286 IleValHisTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsn 305
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    925 ACTGTGCACAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC 984

Qy    306 ProIleLeuTyrAlaPheLeuGlyValAlaLysPheLysSerAlaGlnHisAlaLeuAsn 325
            |||||||||||||||||||||||::::||||||||::::||||||||||||||||||||
Db    985 CCCATCCTCTATGCTTTCCTGGGAGCCAAATTTAAAACCTGCCCAGCACGCACTCACC 1044
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Db    805 AGGACCACAGTCATCCTCATCCTGGCTTTCTGGCTGCCTTACTACATTGGG 864

Qy    266 IleSerIleAspSerPheIleLeuLeuGluIleValIleLysGlyCysAspPheGluSer 285
            |||||||||||||||||||||||||||::::||||||||::::|||||||||||||||
Db    865 ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 924

Qy    286 IleValHisTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsn 305
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    925 ACTGTGCACAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC 984

Qy    306 ProIleLeuTyrAlaPheLeuGlyValAlaLysPheLysSerAlaGlnHisAlaLeuAsn 325
            |||||||||||||||||||||||::::||||||||::::||||||||||||||||||||
Db    985 CCCATCCTCTATGCTTTCCTGGGAGCCAAATTTAAAACCTGCCCAGCACGCACTCACC 1044

Qy    326 SerMetSerArgGlySerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
            |||||||||||||::::|||||||||||::::|||||||||||||||||||||||||
Db    1045 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA 1104

Qy    346 SerValSerThrGluSerGluSerSerSerPheHisSerSer 359
            ||||||||||||||||||||||||||||||||||||||||||
Db    1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC 1146
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RESULT 12
US-08-801-238-3
; Sequence 3, Application US/08801238
Patent No. 5919896
GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1737 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-801-238-3

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Qy     326  SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer   345
                |||:::|||||||||||||||||||||||||||||||||||||||
Db    1045  TCTGTGGAGCAGAGGGTCCAGCCTCCAAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA  1104

Qy     346  SerValSerThrGluSerGluSerSerPheHisSerSer   359
                |||||||||||||||||||||||||||||||||||||||
Db    1105  TCTGTTTCCACTGAGTCTGAGTCTTCAGTTTTCACTCCAGC  1146
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RESULT 13
US-08-801-228-3
; Sequence 3, Application US/08801228
; Patent No. 5922541

GENERAL INFORMATION:
APPLICANT: Lee, James
APPLICANT: Wood, William I.
TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,228
FILING DATE: 19-Feb-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284586
FILING DATE: 10-Aug-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
FILING DATE: 11-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0706P2P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear

US-08-801-228-3

Alignment Scores:
Pred. No.:   9.61e-189   Length: 1737
Score: 1678.50   Matches: 319
Percent Similarity: 95.48%   Conservative: 19
Best Local Similarity: 90.11%   Mismatches: 11
Query Match: 89.90%   Indels: 5
DB: 2   Gaps: 1

US-09-367-052-2 (1-359) x US-08-801-228-3 (1-1737)

```
Qy       6  ValSerIleTyrThrSerAspAsnTyrSerGlyGluValGlySerGlyAspTyrAspSer   25
               ||:||||||||||||||||||||||||||:::|||||||||||||||||||
Db     100  ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGGCTCAGGGGGACTATGACTCC  159

Qy      26  AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr   45
               |||:::|||||||||||||||||||||||||||:::|||||||||||||||||||
Db     160  ATGAGGAGGAACCCTGTTTCCCTGAGCAGAAATGCTAATTTCAATAAAATCTTCCTGCCCACC  219

Qy      46  IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleIleLeuValMet   65
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     220  ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG   279

Qy      66  GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla   85
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     280  GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC   339

Qy      86  AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr  105
               |||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db     340  GACCTCCTCTTCGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC   399

Qy     106  PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     400  TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT   459

Qy     126  ValLeuLeuLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     460  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC   519

Qy     146  SerGlnArgProArgLysLeuLeuAlaGluLysValValGlyValTrpIlePro  165
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     520  AGTCAGAGGCCAAGAAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGGCTCTGGATCCCT  579

Qy     166  AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer  185
               |||||||||||||||||||||||||:::||||||||------AGT
Db     580  GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAAGTC---------AGT  624

Qy     186  GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal  205
               :::      |||||:::|||||:::|||
Db     625  GAGGCAGATGACAGATATCGTGACCGCTTCACCCCAATGACTTGTGGTGGTTGTG   684

Qy     206  PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys  225
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     685  TTCCAGTTTCAGCACATCATGGTTGGCCTTGTATTGTCATCCTGTCCTGC   744

Qy     226  TyrCysIleIleIleSerLeuLeuHisSerHisSerGlyHisHisGlnLysArgLysAlaLeu  245
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     745  TATTTGCATTATCATCTCAAGCTGTCACACTCCAAGGGCCACCAGAAGCCAAGGCCCTC   804

Qy     246  LysThrThrValIleLeuIleLeuAlaPheAlaLysCysTrpLeuProTyrTyrValGly  265
               |||||||||||||||||||||||||||:::||||||||||||||||||||
Db     805  AAGACCACAGTCATCCTCATCCTGGCTTTTGCCAAGTGCTGGCTGCCTTACTACATTGGG   864

Qy     266  IleSerIleAspSerPheLeuLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer  285
               |||||||||||||||||||||||:::|||||||||||||||||||:::|||
Db     865  ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC   924

Qy     286  IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsn  305
               |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     925  ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCACTGTGTCTGAAC   984

Qy     306  ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn  325
               |||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db     985  CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC  1044
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RESULT 14
US-09-104-296-3
; Sequence 3, Application US/09104296
; Patent No. 6087475

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; GENERAL INFORMATION:
;   APPLICANT: Lee, James
;   APPLICANT: Wood, William I.
;   TITLE OF INVENTION: PR4A Receptors
;   NUMBER OF SEQUENCES: 6
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genentech, Inc.
;     STREET: 1 DNA Way
;     CITY: South San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/09/104,296
;     FILING DATE: 24-June-1998
;     CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/701265
;     FILING DATE: 22-AUG-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/664228
;     FILING DATE: 06-JUN-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/076093
;     FILING DATE: 11-JUN-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 07/810782
;     FILING DATE: 19-DEC-1991
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Lové, Richard B.
;     REGISTRATION NUMBER: 34,659
;     REFERENCE/DOCKET NUMBER: P0706P2C2
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 415/225-5530
;     TELEFAX: 415/952-9881
;     TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 1737 base pairs
;     TYPE: Nucleic Acid
;     STRANDEDNESS: Single
;     TOPOLOGY: Linear
US-09-104-296-3

Alignment Scores:
Pred. No.:             9.61e-189
Score:                 1678.50
Percent Similarity:    95.48%
Best Local Similarity: 90.11%
Query Match:           89.90%
DB:                    3
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US-09-367-052-2 (1-359) x US-09-104-296-3 (1-1737)

                                                          Length:       1737
                                                          Matches:      319
                                                          Conservative: 19
                                                          Mismatches:   11
                                                          Indels:       5
                                                          Gaps:         1

Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer   25
         :::|||||||||||||||||||||||||||::||||||||:::|||||||
Db 100 ATCAGTATATACACTTCAGATAACTACACCGGAGGAAATGGGCTCAGGGGACTATGACTCC 159

Qy  26 AsnLysGluProCysPheArgAspArgAsnValHisPheAsnArgIlePheLeuProThr   45
         ||||||||||||||||:::|||||||:::|||||:::|||||||||||||||
Db 160 ATGAAGGAACCCTGTTTCCGTGAACAAAAATGCTAATTTCAATAAAATTCTTCCTGCCCACC 219

Qy  46 IleTyrPheIleIlePheLeuPheGlyLeuValGlyValGlyAsnGlyLeuValIleLeuValMet 65
         |||||||||||||||||||||||||||||||||||||||||||||
Db 220 ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 279

Qy  66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla   85
         ||||||||||||||||||||||||||||||||
Db 280 GGGTTACCAGAAGAAACTGAGAAGCATGACGACAAGTCACGGCTGACCTGTCAGTGGCC 339

Qy  86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr  105
         ||||||||||||||||||::::|||::::||||||||
Db 340 GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC 399

Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
         |||||||||||||||||||||||:::|||||||||||||||
Db 400 TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCACGACAGT 459

Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
         |||||||||||||||||||||||||||||||||||||||
Db 460 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 519

Qy 146 SerGlnArgProArgGlyLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro  165
         |||||||||||||||||||||||||||||||||||:::||||||
Db 520 AGTCAGAGGCCAAGGAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT 579

Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer  185
         |||||||||||||||||||||||||||::|||------------AGT
Db 580 GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAACGTC------------AGT 624

Qy 186 GlnGlyAspAspArgTyrIleCysAspArgTyrProAspSerLeuTrpMetValVal    205
         :::  :::||||||:::|||||||:::||||||||::::|
Db 625 GAGGGCAGATGACAGATATATCTGTGACCGCTTCACCCCAATGACTTGTGGGTGGTTGTG 684

Qy 206 PheGlnPheGlnHisIleMetValGlyLeuProGlyIleValIleLeuSerCys       225
         |||||||||||||||||||||::::||||||||||||||
Db 685 TTCCAGTTTCAGCACATCATGGTGGCCCTTATCCTGGTATTGTCATCCTGTCCTGC 744

Qy 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu  245
         |||||||||||||||||||||||||||||||||||||||||||
Db 745 TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 804

Qy 246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly  265
         |||||||||||||||||||||||||||||||||||::::|
Db 805 AAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGCTGCCTTACTACATTGGG 864

Qy 266 IleSerIleAspSerPhePheLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer  285
         ||||||||||||||||||||||||::::|||||||:::||||||
Db 865 ATCAGCATCGACTCCTTCTTCCTCCTGGAAATCATCAAGCAAGGTGTGAGTTTGAGAAC 924

Qy 286 IleValHisHisTyrTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsn  305
         ||||||||||||||||||||||||||||||||||||||||||
Db 925 ACTGTGCACAAGTGGATTTCCATCACGGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC 984

Qy 306 ProIleLeuTyrAlaPheLeuGlyGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
         |||||||||||||||||||||||||||||||||||||
Db 985 CCCATCCTCTATGCTTTCCTTGGAGGCAAATTTAAAACCTCTGCCCAGCACGCACTCACC 1044

Qy 326 SerMetSerArgGlySerLeuLysIleLeuSerLysLysGlyLysArgGlyGlyHisSer  345
         |::::|||:::|||||||||||||||||||||||||
Db 1045 TCTGTGCAGCAGGGGTCCAGCTCCAGATCCTCTCCAAAGGAAAGCGGAGGTGGACATTCA 1104

Qy 346 SerValSerThrGluSerSerSerPheHisSerSer                         359
         ||::::|||||||||||||||||||
Db 1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC 1146
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         STATE: California
       COUNTRY: USA
           ZIP: 94080
COMPUTER READABLE FORM:
   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06380
  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/076093
  FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
          NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2P1
TELECOMMUNICATION INFORMATION:
     TELEPHONE: 415/225-5530
       TELEFAX: 415/952-9881
         TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:  2:
SEQUENCE CHARACTERISTICS:
        LENGTH: 1737 bases
          TYPE: nucleic acid
   STRANDEDNESS: single
      TOPOLOGY: linear
PCT-US94-06380-2
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Alignment Scores:
Pred. No.:                9.61e-189      Length:           1737
Score:                    1678.50        Matches:           319
Percent Similarity:       95.48%         Conservative:       19
Best Local Similarity:    90.11%         Mismatches:         11
Query Match:              89.90%         Indels:              5
DB:                                      Gaps:                1
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US-09-367-052-2 (1-359) x PCT-US94-06380-2 (1-1737)

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Qy     6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer  25
           ::|||||:||||||||||||||||||||:|||:|||||||||||||:|||||||||||
Db   100 ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGGCTCAGGGGACTATGACTCC 159

Qy    26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr  45
           |||||||||||||||||::|||||   ::|||||||||||||||:::||||||||||
Db   160 ATGAAGGAACCCCGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC 219

Qy    46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet  65
           ||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db   220 ATCTACTTCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 279

Qy    66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla  85
           ||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db   280 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC 339

Qy    86 AspLeuPheValIleThrLeuProPheTrpLeuProAlaValAlaMetAlaAspTrpTyr 105
           ||||||||||||||||||||||||||||||||||||||:||:|||||||||||||
Db   340 GACCTCTTCGTCATCACGCTTCCCTTCTGGCTCCCTGCAGTGGCAAATGGCTGACTGGTAC 399

Qy   106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
           |||||||||||||||||||||||||||||||||||||||||||||:::||||||||
Db   400 TTTGGGAAGTTCCTATGCAAGGCAGTCCATATCATCTACACAGTCAACCTCTACAGCAGT 459

Qy   126 ValLeuLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   460 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 519

Qy   146 SerGlnArgProArgLeuLeuAlaGluValLysAlaValTyrValGlyValTrpIlePro 165
           |||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Db   520 AGTCAGAGGCCCAAGGAACTGTTGGCTGAAGTGAAAGCTGTTTATGTTGGCGTCTGGATCCCT 579
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Qy       AlaLeuLeuLeuThrIleProPheIlePheAlaAlaValSerGlnGlyAspIleSer 185
           ||||||||||||||||||||||||||||||||||||||||::|
Db   580 GCCCTCCTGCTGACTATTCCGACTTCATCTTCGCAGCGTC---------AGT 624

Qy   186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
           :::||||||||||||||||||||||:::|||||||||||||||:::
Db   625 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCATGACTTGTGGGTGGTTGTG 684

Qy   206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSerCys 225
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   685 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC 744

Qy   226 TyrCysIleIleIleSerLysHisSerHisSerLysHisGlnLysArgLysAlaLeu 245
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   745 TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 804

Qy   246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
           :::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   805 AAGACCACAGTCATCCTCATCCTGCTTTCTCGCCTGTGGCCTGCCTTACTACATTGGG 864

Qy   266 IleSerIleAspSerPheIleLeuLeuGluIleLysGlnGlyCysAspPheGluSer 285
           |||||||||||||||||||||||||||  :::||||||||||||||||||||
Db   865 ATCAGCATGGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 924

Qy   286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   925 ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC 984

Qy   306 ProLeuLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   985 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC 1044

Qy   326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyGlyArgGlyGlyHisSer 345
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1045 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA 1104

Qy   346 SerValSerThrGluSerSerSerPheHisSerSer 359
           ||||||||||||||||||||||||||||||||||
Db  1105 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC 1146
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Search completed: January 11, 2006, 00:32:36
Job time : 300 secs

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                    GenCore version 5.1.6
         Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:     January 11, 2006, 00:22:05 ; Search time 1042 Seconds
                                     (without alignments)
                                     2849.047 Million cell updates/sec

Title:         US-09-367-052-2
Perfect score: 1867
Sequence:      1 MEPISVSIYTSDNYSEEVGS.........KRGGHSSVSTESESSSFHSS 359

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters:    19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09367052/runat_10012006_102843_10231/app_query.fasta_1.519
-DB=Published_Applications_NA_Main -QMT=fastap -SUFFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09367052 @CGN_1_1.026 @runat_10012006_102843_10231 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications NA_Main:*
    1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
    2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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    9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
   10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

                              SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the total score of the result being printed,
and is derived by analysis of the total score distribution.
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	1867	100.0	1758	8	US-10-785-230-4	Sequence 4, Appli
2	1744.5	93.4	1050	8	US-10-486-706-54	Sequence 54, Appl
3	1678.5	89.9	1059	3	US-09-813-651B-84	Sequence 84, Appl
4	1678.5	89.9	1059	6	US-10-014-322A-125	Sequence 125, App
5	1678.5	89.9	1059	8	US-10-160-401-2	Sequence 2, Appli
6	1678.5	89.9	1059	8	US-10-775-920-375	Sequence 375, App
7	1678.5	89.9	1059	9	US-10-929-182-8	Sequence 8, Appli

8	1678.5	89.9	1059	9	US-10-985-324-1	Sequence 1, Appli
9	1678.5	89.9	1225	6	US-10-101-510-741	Sequence 741, App
10	1678.5	89.9	1225	6	US-10-305-720-1235	Sequence 1235, Ap
11	1678.5	89.9	1588	8	US-10-775-920-370	Sequence 370, App
12	1678.5	89.9	1637	8	US-10-785-230-2	Sequence 2, Appli
13	1678.5	89.9	1645	8	US-10-775-920-372	Sequence 372, App
14	1678.5	89.9	1645	8	US-10-775-920-374	Sequence 374, App
15	1678.5	89.9	1662	7	US-10-505-680-185	Sequence 185, App
16	1678.5	89.9	1664	7	US-10-706-265-11	Sequence 11, Appl
17	1678.5	89.9	1664	7	US-10-641-643-1213	Sequence 1213, Ap
18	1678.5	89.9	1670	3	US-10-775-920-369	Sequence 369, App
19	1678.5	89.9	1670	3	US-09-880-107-2143	Sequence 2143, App
20	1678.5	89.9	1670	3	US-09-960-706-636	Sequence 636, App
21	1678.5	89.9	1670	3	US-10-372-683-1	Sequence 1, Appli
22	1678.5	89.9	1670	7	US-10-440-464-77	Sequence 77, Appl
23	1678.5	89.9	1670	7	US-10-717-597-317	Sequence 317, App
24	1678.5	89.9	1670	5	US-10-775-920-367	Sequence 367, App
25	1678.5	89.9	1679	5	US-10-151-274-14	Sequence 14, Appl
26	1678.5	89.9	1679	5	US-10-225-567A-75	Sequence 75, Appl
27	1678.5	89.9	1679	5	US-10-021-660-58	Sequence 58, Appl
28	1678.5	89.9	1679	6	US-10-170-385-332	Sequence 332, App
29	1678.5	89.9	1679	6	US-10-341-434-177	Sequence 177, App
30	1678.5	89.9	1679	6	US-10-172-118-912	Sequence 912, App
31	1678.5	89.9	1679	7	US-10-211-462-80	Sequence 80, Appl
32	1678.5	89.9	1679	7	US-10-181-906-9	Sequence 9, Appli
33	1678.5	89.9	1679	8	US-10-342-887-912	Sequence 912, App
34	1678.5	89.9	1679	8	US-10-775-920-366	Sequence 366, App
35	1678.5	89.9	1679	8	US-10-278-698-64	Sequence 64, Appl
36	1678.5	89.9	1679	9	US-10-278-698-578	Sequence 578, App
37	1678.5	89.9	1679	9	US-10-888-313A-62	Sequence 62, Appl
38	1678.5	89.9	1679	9	US-10-486-471-19	Sequence 19, Appl
39	1678.5	89.9	1699	3	US-10-775-920-373	Sequence 373, App
40	1678.5	89.9	1711	3	US-09-971-392-20	Sequence 20, Appl
41	1678.5	89.9	1711	6	US-10-101-510-459	Sequence 459, App
42	1678.5	89.9	1737	3	US-09-104-063-3	Sequence 3, Appli
43	1678.5	89.9	1737	7	US-10-666-689-3	Sequence 3, Appli
44	1678.5	89.9	1826	8	US-10-723-860-5773	Sequence 5773, Ap
45	1672.5	89.6	1059	3	US-09-826-509-484	Sequence 484, App

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                              ALIGNMENTS

RESULT 1
US-10-785-230-4
; Sequence 4, Application US/10785230
; Publication No. US2004209937A1
; GENERAL INFORMATION:
;  APPLICANT: KISHIMOTO, Tadamitsu
;  APPLICANT: NAGASAWA, Takashi
;  APPLICANT: TACHIBANA, Kazunobu
;  APPLICANT: CHUGAI SEIYAKU KABUSIKI KAISHA
;  TITLE OF INVENTION: Vascularization Inhibitors
;  FILE REFERENCE: 46124-5042-US
;  CURRENT APPLICATION NUMBER: US/10/785,230
;  CURRENT FILING DATE: 2004-02-25
;  PRIOR APPLICATION NUMBER: PCT/JP99/01448
;  PRIOR FILING DATE: 1999-03-23
;  PRIOR APPLICATION NUMBER: JP10/95448
;  PRIOR FILING DATE: 1998-03-24
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
;  LENGTH: 1758
;  TYPE: DNA
;  ORGANISM: Mus
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(1080)
;  OTHER INFORMATION:
US-10-785-230-4

Alignment Scores:
Pred. No.:      1.12e-196            Length:      1758
Score:          1867.00             Matches:      359
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Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: Gaps: 8

US-09-367-052-2 (1-359) x US-10-785-230-4 (1-1758)

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Qy     1 MetGluProIleLeuSerValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySer 20
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Db     1 ATGGAACCGATCAGTGTGAGTATATACACTTCTGATAACTACTCTGAAGAAGTGGGGTCT 60

Qy    21 GlyAspTyrAspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsnArg 40
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Db    61 GGAGACTATGACTCCAACAAGGAACCCTGCTTCCGGGATGAAAACGTCCATTTCAATAGG 120

Qy    41 IlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeu 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ATCTTCCTTCCCACCATCTACTTCATCATCTTCTTGACTGGCATAGTGGGCAATGGATTG 180

Qy    61 ValIleLeuValMetGlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeu 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GTGATCCTGGTCATGGGTTACCAGAAGAAGCTAAGGAGCATGACGGACAAGTACCGGCTG 240

Qy    81 HisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAla 100
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Db   241 CACCTGTCAGTGGCTGACCTCCTTTGTCATCACACTCCCTTTCTGGGCAGTTGATGCC 300

Qy   101 MetAlaAspTrpTyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrVal 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 ATGGCCGACTGGTACTTTGGGAAATTTTGTAAGGCTGTCCATATCATCTACACTGTC 360

Qy   121 AsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIle 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AACCTCTACAGCAGCGTTCTCATCCTGGCTTCATCAGCCTGGACCCGGTACCTCGCCATT 420

Qy   141 ValHisAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGluLysValAlaValTyrVal 160
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Db   421 GTCCACGCCACCAACAGTCAAAGGCCAAGGAAGCTGCTGGCTGAAAAGGCAGTCTATGTG 480

Qy   161 GlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePheAlaAlaAspValSer 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGCGTCTGGATCCCAGCCCTCCTCCTGACTATACCTGACTTCATCTTTGCCGACGTCAGC 540

Qy   181 GlnGlyAspIleSerGlnGlyAlaAspArgTyrIleCysAspArgLeuTyrProAspSer 200
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Db   541 CAGGGGGACATCAGTCAGGGGGCAGACAGATACATCTGTGACCGGCTTTACCCCGATAGC 600

Qy   201 LeuTrpMetValValPheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIle 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CTGTGGATGGTGGTGTTTCAATTCCAGCATATAATGGTGGGTCTCATCCTGCCCGGCATC 660

Qy   221 ValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGln 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GTCATCCTCTCCTGTTACTGCATCATCATCTCTAAGCTGTCACACTCCAAGGGCCACCAG 720

Qy   241 LysArgLysAlaLeuLysThrThrValIleLeuLeuLeuAlaPhePheAlaCysTrpLeu 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 AAGCGCAAGGCCCTCAAGACGACCGTCATCCTGCTCCTAGCTTTCTTTGCCTGCTGGCTG 780

Qy   261 ProTyrTyrValGlyIleSerIleAspSerPheIleLeuLeuGluGlyValIleLysGlnGly 280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 CCATATTATGTGGGAATCAGCATCGACTCCTTCATCCTTTTGGGAGTCATCAAGCAAGGA 840

Qy   281 CysAspPheGluAsnValHisTrpIleSerIleThrGluAlaLeuAlaLeuAlaPhePhe 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TGTGACTTCGAGAACGTTCACTGGATCTCCATCACAGAGGCCCTTGCCCTTGCCTTCTTC 900

Qy   301 HisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla 320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901 CACTGTTGCCTGAACCCCATCCTCTATGCCTTCCTGGGGGCCAAGTTCAAAAGCTCTGCC 960

Qy   321 GlnHisAlaLeuAsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLys 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   961 CAGCATGCACTCAACTCCATGAGCAGAGGCTCCAGCCTCAAGATCCTTTCCAAAGGAAAG 1020

Qy   341 ArgGlyGlyHisSerSerValSerThrGluSerGluSerSerSerPheHisSerSer 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1021 CGGGGTGGACACTCTTCCGTCTCCACGGAGTCAGAATCCTCCAGTTTCACTCAGC 1077
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RESULT 2
US-10-486-706-54
; Sequence 54, Application US/10486706
; Publication No. US2005007108BA1
; GENERAL INFORMATION:
; APPLICANT: LANDFIELD, PHILIP W.
; APPLICANT: BLALOCK, ERIC M.
; APPLICANT: CHEN, KUEY-CHU
; APPLICANT: FOSTER, THOMAS C.
; TITLE OF INVENTION: GENE EXPRESSION PROFILE BIOMARKERS AND THERAPEUTIC TARGETS FOR
; TITLE OF INVENTION: BRAIN AGING AND AGE-RELATED COGNITIVE IMPAIRMENT
; FILE REFERENCE: 50229-426
; CURRENT APPLICATION NUMBER: US/10/486,706
; CURRENT FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: PCT/US02/25607
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 60/311,343
; PRIOR FILING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 1050
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-486-706-54

Alignment Scores:
Pred. No.:   Length: 1050
Score: 2.16e-183   Matches: 338
                           1744.50   Conservative: 4
Percent Similarity: 96.61%   Mismatches: 7
Best Local Similarity: 95.48%   Indels: 5
Query Match: 93.44%   Gaps: 1
DB: 9

US-09-367-052-2 (1-359) x US-10-486-706-54 (1-1050)

```
Qy     6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
           :::    ::: |||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGGAAAATATACACTTCGGATAACTACTCCGAAGAAGTAGGGTCTGGAGACTATGACTCC 60

Qy    26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
           ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    61 AACAAGGAACCCTGCTTCCGGGATGAAAACGAAAACTTCAACAGGATCTTCCTGCCCACC 120

Qy    46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
           ||||||||||||| |||||||||||||||| |||||||||||||||||||||||||||||
Db   121 ATCTATTTTATCATCTTCTTGACTGGCATAGTGGGCAATGGTTGTAATCCTGGTCATG 180

Qy    66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 GGTTACCAGAAGAAGCTGAGGAGCATGACAGAGAAGTACCGGCTGCACCTGTCCGTGGCT 240

Qy    86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GACCTCCTCTTTGTCATCACACTCCCCTTCTGGGCAGTGGACGCCATGGCTGACTGGTAC 300

Qy   106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TTTGGGAAATTTTTATGTAAGGCTGTCCATATCATCTACACAGTCAACCTTTACAGCAGT 360

Qy   126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTTCTCATCCTGGCCTTCATCAGCCTGGACCGCTACCTTGCCATTGTCCACGCCACCAAC 420

Qy   146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGCCAGAGGCCGCGGAAGCTGCTGGCTGAAAAGGCCGTCTATGTGGGTGTCTGGATCCCC 480
```

```
Pred. No.:
Score:                    1678.50       Length:        1059
                          4.81e-176     Matches:        319
Percent Similarity:       95.48%        Conservative:    19
Best Local Similarity:    90.11%        Mismatches:      11
Query Match:                            Gaps:             5
DB:                           3                           1
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US-09-367-052-2 (1-359) x US-09-813-651B-84 (1-1059)

```
Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluGlnGluValGlySerGlyAspTyrAspSer  25
         :::||||||||||||||::||||||||||
Db  10 ATCAGTATATACACTTCAGATAACTACACCAGGAGAAATGGGTCAGGGACTATGACTCC      69

Qy  26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr     45
         |||||||||||:::|||||:|||||||
Db  70 ATGAGGAGGACCCCTGTTTCCGTGAAGAAGATGTCAATTAATAAAATCTTCCTGCCCACC    129

Qy  46 IleTyrPheIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet        65
         ||||||||||||||||||||||||||
Db 130 ATCTACTTCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG    189

Qy  66 GlyTyrGlnLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla        85
         |||||||||||||||||||||||||
Db 190 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC    249

Qy  86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr    105
         ||||||||||||||||||||||||||
Db 250 GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC    309

Qy 106 PheGlyLysPheLeuCysLysValAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
         ||||||||||||||||:::|||||||
Db 310 TTTGGAAACTTCCTATGCAAGGCAGTCCATCATCTACACAGTCAACCTCTACAGCAGT      369

Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn   145
         ||||||||||||||||||||||||||
Db 370 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC    429

Qy 146 SerGlnArgProArgLysLeuLeuAlaGluLysValValTyrValGlyValTrpIlePro   165
         ||||||||||||||||||||||||||
Db 430 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT    489

Qy 166 AlaLeuLeuLeuThrIleProAspPhePheAlaAspValSerGlnGlyAspIleSer      185
         ||||||||||||||||||::|||
Db 490 GCCCTCCTCCTGACTATCCCGACTTCATCTTTGCCAACGTC------AGT             534
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```
Qy 166 AlaLeuLeuThrIleProAspPhePheAlaAspValSerGlnGlnGlyAspIleSer      185
         ||||||||||||||||||||||||
Db 481 GCCCTCCTCCTGACTATCCCGACTATCATCTTTGCCGATGTC--------AGC          525

Qy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal   205
         ||||||||||||||||||||||||||
Db 526 CAGGGGGACGGACCAGTACATCTGTGACCGCCTTTACCCGGACAGCCTGTGGATGGTGGTG  585

Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys   225
         ||||||||||||||||||||||||||
Db 586 TTCCAGTTTCAGCACATCATGGTGGGCCTGGTATTGTCATCCTGTCCTGC             645

Qy 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu   245
         ||||||||||||||||||||||||||
Db 646 TACTGCATCATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC    705

Qy 246 LysThrThrValIleLeuIleLeuAlaPheLeuAlaCysTrpLeuProTyrTyrValGly   265
         ||||||||||||||||||||||||||
Db 706 AAGACTACGGTCATCCTTATCCTGGCTTTCCTGGCCTGCTGGCTACCGTATTACGTGGGG    765

Qy 266 IleSerIleAspSerPheIleLeuLeuGluIleIleLysGlnGlyCysGluPheGluSer   285
         ||||||||||||||::::||||||||
Db 766 ATCAGCATCGATTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC    825

Qy 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn   305
         ::|||||||||||||||||||||
Db 826 ATCGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC    885

Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn   325
         |||||||||||||||||:::|||||||
Db 886 CCCATCCTCTACGCCTTCCTCGGGGCCAAATTCAAGAGCTCCGCGCAGCATGCCACTCAT    945

Qy 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer   345
         ||||||||||||||||||||||||||
Db 946 TCCATGAGCAGAGGCTCCAGCCTCAAGATCCTTTCCAAAGGGAAACGGGGTGGACACTCT   1005

Qy 346 SerValSerThrGluSerGluSerSerSerPheHisSerSer                     359
         |||||||||||||||
Db 1006 TCCGTCTCCACAGAGTCAGAATCCTCAGTTTCACTCCAGC                      1047
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Alignment Scores:

Qy   326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
          |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   955 TCTGTGAGCAGAGAGGGTCCAGCCTCCAAGATCCTCCAAAGGAAAGCGAGGTGGACATTCA 1014

Qy   346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
          |||||||||||||||||||||||||||||||||||||||
Db 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC 1056

RESULT 4
US-10-014-322A-125
; Sequence 125, Application US/10014322A
; Publication No. US20030167129A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, Jr., John
; APPLICANT: Wilson, Carol
; APPLICANT: Tan Hehir, Christina
; APPLICANT: Kates, Steven
; APPLICANT: Krstenansky, John
; TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
; FILE REFERENCE: CNS-008
; CURRENT APPLICATION NUMBER: US/10/014,322A
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/243,587
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 09/813,651
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 09/813,653
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 09/813,448
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 126
; SEQ ID NO 125
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1059)
; OTHER INFORMATION: human CXCR4 gene
US-10-014-322A-125

Alignment Scores:
Pred. No.:   4.8le-176
Score: 1678.50
Percent Similarity: 95.48%
Best Local Similarity: 90.11%
Query Match: 89.90%
DB: 6

Length:	1059	Matches:	319
		Conservative:	19
		Mismatches:	11
		Indels:	5
		Gaps:	1

US-09-367-052-2 (1-359) x US-10-014-322A-125 (1-1059)

Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer 25
         |:|||||||||||||||||||||:::|||||||||::::|||||||||||
Db   10 ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGCTCAGGGACTATGACTC 69

Qy   26 AsnLysGluProCysPheArgPheAspGluAsnValHisPheAsnValIleProThr 45
         :::|||||||||| ::|||||||||||||||||:::|||||
Db   70 ATGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCGTGCCCACC 129

Qy   46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 130 ATCTACTTCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 189

Qy   66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
         |||||||||||||||||||||||||||||||||||||||||||||
Db 190 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC 249

Qy   86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
         |||||||||||||||| ||||||||||||||:::||||||
Db 250 GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC 309

Qy 106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125

Db   310 TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTTCACAGCAGT 369

Qy   126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
          |||||||||||||||||||||||||||||||||||||||||||||||||----------AGT 534
Db   370 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 429

Qy   146 SerGlnArgProArgLysArgLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
          |||||||||||||||||||||||||||||||||||||||||||||
Db   430 AGTCAGAGGCCAAGGAAGCGTGTTGGCTGAAAAGGTGGTCTATGTGGGCGTCTGGATCCCT 489

Qy   166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnAspGlyAspIleSer 185
          |||||||||||||||||||||||||||||||||||||||||:::||
Db   490 GCCCTCCTGCTGACTATCCCGACTTCATCTTTGCCAGGTC----------AGT 534

Qy   186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
          ::: ||||||||||||||||||||| |||:|||||||||||||
Db   535 GAGGCAGATGACAGATATATCTGTGACCGGCTTCTACCCCAATGACTTGTGGTGGTTGTG 594

Qy   206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
          ||||||||||||||||||||||||||||||||||||||||||||
Db   595 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC 654

Qy   226 TyrCysIleIleIleSerLysHisSerLysGlyHisGlnLysArgLysValAlaLeu 245
          |||||||||||||||||||||||||||||||||||||||||||||||
Db   655 TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 714

Qy   246 LysThrThrValIleLeuIleLeuAlaPheAlaCysTrpLeuProTyrTyrValGly 265
          |||||||||||||||||||||||||||||||||||||::::||
Db   715 AAGACCACAGTCATCTTGATCCTGGCTTTTGCCTGTTGGCTGCCTTACTACTATGGG 774

Qy   266 IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysGluPheGluSer 285
          :::||||||||||||||||||||||||||||||||
Db   775 ATCAGCATCGACTCCTTCATCCTCCTGGGAAATCATCAAGCAAGGGGTGTGAGTTTGAGAAC 834

Qy   286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   835 ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC 894

Qy   306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
          |||||||||||||||||||||||||||||:::|||||||
Db   895 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC 954

Qy   326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
          |||:::|||||||||||||||||||||||||||||||||||||||
Db   955 TCTGTGAGCAGAGAGGGTCCAGCCTCCAAGATCCTCCAAAGGAAAGCGAGGTGGACATTCA 1014

Qy   346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
          |||||||||||||||||||||||||||||||||||||||
Db 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC 1056

RESULT 5
US-10-160-401-2
; Sequence 2, Application US/10160401
; Publication No. US20030207281A1
; GENERAL INFORMATION:
; APPLICANT: Genaissance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Bieglecki, Karyn M.
; APPLICANT: Koshy, Beena
; APPLICANT: Monroe, Glen
; APPLICANT: Rounds, Eileen
; TITLE OF INVENTION: HAPLOTYPES OF THE CXCR4 GENE
; FILE REFERENCE: MWH-0121US
; CURRENT APPLICATION NUMBER: US/10/160,401
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: PCT/US01/12268
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/197,025
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

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;  LENGTH: 1059
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-160-401-2

Alignment Scores:
Pred. No.:              4.81e-176      Length:          1059
Score:                  1678.50        Matches:         319
Percent Similarity:     95.48%         Conservative:    19
Best Local Similarity:  90.11%         Mismatches:      11
Query Match:                           Indels:          5
DB:                                    Gaps:            1

US-09-367-052-2 (1-359) x US-10-160-401-2 (1-1059)

Qy      6 ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer      25
            :::||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db     10 ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGGCTCAGGGGACTATGACTCC   69

Qy     26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr   45
            |||||||||||||||||||||||||| :::||||||||||||||||||||||||||||
Db     70 ATGAAGGAACCCCGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC  129

Qy     46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet   65
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG  189

Qy     66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla   85
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC  249

Qy     86 AspLeuLeuPheValIleThrLeuProPheThrLeuAlaValAlaAspAlaMetAlaAspTrpTyr  105
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GACCTCCTCTTTGTCATCACGCTTCCCTTCCCTCTGGCAGTTGATGCCGTGGCAAACTGGTAC  309

Qy    106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
            |||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db    310 TTTGGAAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT  369

Qy    126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC  429

Qy    146 SerGlnArgProArgLysLeuLeuAlaGluLysGlyValTyrValGlyValTrpIlePro  165
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    430 AGTCAGAGGCCCAAGGAGCTGTTGGCTGAAAAAGGTGGTCTATGTGGCGTCTGGATCCCT  489

Qy    166 AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnAspIleSer        185
            ||||| ||||||||||||||||||||||||||||||||||||||:::|||||||
Db    490 GCCCTCCTGACTATTCCCGACTTCATCTTTGCCAACGTC----------AGT  534

Qy    186 GlnGlyPheIleAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal  205
            :::  ||||||||||||||||||||||||||||||||||||||||:::||||||||
Db    535 GAGGCAGATGACAGATATATCTGTGACCGGCTTCTACCCGACTTGTGGGGTGGTTGTG   594

Qy    206 PheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValLeuLeuSerCys  225
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    595 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC  654

Qy    226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu  245
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    655 TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC  714

Qy    246 LysThrThrValIleLeuIleLeuAlaPheAlaCysTrpLeuProTyrTyrValGly    265
            :::||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db    715 AAGACCACAGTCATCCTCATCCTGGCTTTCGCCTGCTGGCTCCCTTACTACATTGGG  774

Qy    266 IleSerIleAspSerPheIleLeuLeuGluValIleLysGlnGlyCysAspPheGluSer  285
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    775 ATCAGCATCGACTCCTTCATCCTCCTGGAAGTCATCAAGCAAGGGTGTGAGTTTGAGAAC  834

Qy    286 IleValHisLysTrpIleSerIleThrGluIleLeuAlaLeuAlaPheCysGlnLeuAsn  305
            |||||||||||||||||||||||||
Db    835 ATCGTGCACAAGTGGATTTCCATCACCGAGATCCTGGCCCTAGCTTTCTTCCACTGTGTCTGAAC  894
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Second column:

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Db    835 ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTGTCTGAAC  894

Qy    306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheSerSerAlaGlnHisAlaLeuAsn    325
            |||||||||||||||||||||||||||| :::||||||||||||||||||||
Db    895 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCCACTCACC  954

Qy    326 SerMetSerArgGlySerSerLeuLysSerLeuSerIleLysGlyLysArgGlyGlyHisSer  345
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    955 TCTGTGAGCAGAGGGTCCAGCTCTCAAGATCCTCTCCAAAGGAAGCGAGGTGGACATTCA  1014

Qy    346 SerValSerThrGluSerGluSerSerSerPheHisSerSer    359
            ||||||||||||||||||||||||||||||||||||||||||
Db   1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC  1056
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RESULT 6
US-10-775-920-375
;  Sequence 375, Application US/10775920
;  Publication No. US20040175744A1
;  GENERAL INFORMATION:
;  APPLICANT: Mergen Ltd
;  TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
;  TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
;  TITLE OF INVENTION: IN CERTAIN CANCERS
;  FILE REFERENCE: Mergen - 0010B
;  CURRENT APPLICATION NUMBER: US/10/775,920
;  CURRENT FILING DATE: 2004-02-10
;  PRIOR APPLICATION NUMBER: US 60/447,900
;  PRIOR FILING DATE: 2003-02-13
;  NUMBER OF SEQ ID NOS: 385
;  SOFTWARE: Patentin version 3.2
;  SEQ ID NO 375
;  LENGTH: 1059
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-775-920-375

Alignment Scores:
Pred. No.:              4.81e-176      Length:          1059
Score:                  1678.50        Matches:         319
Percent Similarity:     95.48%         Conservative:    19
Best Local Similarity:  90.11%         Mismatches:      11
Query Match:                           Indels:          5
DB:                                    Gaps:            1

US-09-367-052-2 (1-359) x US-10-775-920-375 (1-1059)

Qy      6 ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer      25
            :::||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db     10 ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGGCTCAGGGGACTATGACTCC   69

Qy     26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr   45
            |||||||||||||||||||||||||| :::||||||||||||||||||||||||||||
Db     70 ATGAAGGAACCCCGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC  129

Qy     46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet   65
            ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG  189

Qy     66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla   85
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC  249

Qy     86 AspLeuLeuPheValIleThrLeuProPheThrLeuAlaValAlaAspAlaMetAlaAspTrpTyr  105
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    250 GACCTCCTCTTTGTCATCACGCTTCCCTTCCCTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC  309

Qy    106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
            |||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db    310 TTTGGAAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT  369

Qy    126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    370 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC  429
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DB:

US-09-367-052-2 (1-359) x US-10-929-182-8 (1-1059)

Qy   9   Gaps: 1

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Qy     6  ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer  25
Db    10  ATCAGTATATACACTTCAGATAACTACACGGAAGAAATGGGCTCAGGGACTATGACTCC  69

Qy    26  AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr  45
Db    70  ATGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC  129

Qy    46  IleTyrPheIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet  65
Db   130  ATCTACTTCATCATCTTCTTAACTGGCATTGTGGGCAATGGTCATCCTGGTCATG  189

Qy    66  GlyTyrArgLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla  85
Db   190  GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC  249

Qy    86  AspLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr  105
Db   250  GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC  309

Qy   106  PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
Db   310  TTTGGAAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT  369

Qy   126  ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
Db   370  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC  429

Qy   146  SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro  165
Db   430  AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT  489

Qy   166  AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer  185
Db   490  GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAACGTC----------AGT  534

Qy   186  GlnGlyAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal  205
Db   535  GAGGCAGATGACAGATATCGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTTGTG  594

Qy   206  PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys  225
Db   595  TTCCAGTTCCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC  654

Qy   226  TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu  245
Db   655  TATTGCATTATAATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC  714

Qy   246  LysThrValIleLeuIleLeuAlaPheLeuAlaCysTrpLeuProTyrTyrValGly  265
Db   715  AAGACCACAGTCATCCTCATCCTGGCTTTCTCGCGCTGCTTTGGCCTCCGTGGTGTG  774

Qy   266  IleSerIleAspSerPheIleLeuLeuGluIleIleLysGlnGlyCysAspPheGluSer  285
Db   775  ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC  834

Qy   286  IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsn  305
Db   835  ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCTGCTGTCTGAAC  894

Qy   306  ProLeuLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn  325
Db   895  CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC  954

Qy   326  SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyGlyHisSer  345
Db   955  TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA  1014

Qy   346  SerValSerThrGluSerGluSerSerSerPheHisSerSer  359
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RESULT 7
US-10-929-182-8

Alignment Scores:

Pred. No.:		
Score:	4.8e-176	Length: 1059
Score:	1678.50	Matches: 319
Percent Similarity:	95.48%	Conservative: 19
Best Local Similarity:	90.11%	Mismatches: 11
Query Match:	89.90%	Indels: 5

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Db 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC 1056
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RESULT 8
US-10-985-324-1
; Sequence 1, Application US/10985324
; Publication No. US20050202019A1
; GENERAL INFORMATION:
; APPLICANT: Northwest Biotherapeutics, Inc.
; APPLICANT: Murphy, Gerald P.
; APPLICANT: Boynton, Alton L.
; APPLICANT: Sehgal, Anil
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC APPLICATIONS BASED ON THE
; TITLE OF INVENTION: ROLE OF THE CXCR-4 GENE IN TUMORIGENESIS
; FILE REFERENCE: 20093-000600PC
; CURRENT APPLICATION NUMBER: US/10/985,324
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US/09/647,501
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/079,916
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/104,656
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 1
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-985-324-1

Alignment Scores:
Pred. No.:
Score: 4.81e-176
                        1678.50
Percent Similarity: 95.48%
Best Local Similarity: 90.11%
Query Match: 89.90%
DB:

Length: 1059
Matches: 319
Conservative: 19
Mismatches: 11
Indels: 5
Gaps: 9

US-09-367-052-2 (1-359) x US-10-985-324-1 (1-1059)

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Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer  25
         :::||||||||||||||||||||||||||:::||||||::|
Db  10 ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGGCTCAGGGACTATGACTCC   69

Qy  26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr  45
         ||||||||||||:::||||||||:::|:::|||
Db  70 ATGAGGAAGGACCCTGTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCAC 129

Qy  46 IleTyrPheIlePheIleLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet  65
Db 130 ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 189

Qy  66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla  85
Db 190 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC 249

Qy  86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 250 GACCTCCTTTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC 309

Qy 106 PheGlyLysPhePheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer 125
Db 310 TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT 369

Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 370 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 429

Qy 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
Db 430 AGTCAGAGGCCCAAGGAGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT 489
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Qy 166 AlaLeuLeuLeuThrIleProAsnPheIlePheAlaAspValSerGlnGlyAspIleSer 185
         ||||||||||||||||||||||||||||||||||:::|||
Db 490 GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAAGGTC------------AGT 534

Qy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
         ||||||:::||||||||::||
Db 535 GAGGCAGATGACAGATATATCTGTGACCGCTTCTACCCCAATGACTTGTGGGTGGTTGTG 594

Qy 206 PheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleLeuValIleLeuSerCys 225
         |||||||||||||||||||||||||||||||||||||||:::||||||
Db 595 TTCCAGTTCCAGCACATCATGGTTGGCCCTATCCTGGTATTGTCATCCTGTCCTGC 654

Qy 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 655 TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 714

Qy 246 LysThrThrValIleLeuLeuLeuAlaPheAlaCysTrpLeuProTyrTyrValGly 265
         ||||||||||||||||||||||||||||||||||||||||||||||:::|
Db 715 AAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGCTGCCTTACTACATTGGG 774

Qy 266 IleSerIleAspSerPheLeuLeuLeuGluIleValIleLysGlnGlyCysAspPheGluSer 285
         |||||||||||          :::|||||||||||||||:::|||
Db 775 ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTGAGAAC 834

Qy 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsn 305
Db 835 ACTGTGCACAAGTGGATTTCCATCACCGAGCCCTAGCTTTCTTCCTACTGTGTCTGAAC 894

Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheSerSerAlaGlnHisAlaLeuAsn 325
Db 895 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC 954

Qy 326 SerMetSerArgGlySerLeuLysIleLeuSerLysLysGlyLysArgGlyHisSer 345
         ||||:::|||||||||||||||||||||||||||||
Db 955 TCTGTGAGCAGAGGGTCCAGCTCAAGATCCTCTCCAAAGAAGAAAGGGAGGTGGGACATTCA 1014

Qy 346 SerValSerThrGluSerGluSerSerPheHisSerSer 359
Db 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC 1056
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RESULT 9
US-10-101-510-741
; Sequence 741, Application US/10101510
; Publication No. US2003014 8295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 741
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-741

Alignment Scores:
Pred. No.:
Score: 6.02e-176
                        1678.50
Percent Similarity: 95.48%
Best Local Similarity: 90.11%
Query Match: 89.90%
DB:

Length: 1225
Matches: 319
Conservative: 19
Mismatches: 11
Indels: 5
Gaps: 1

US-09-367-052-2 (1-359) x US-10-101-510-741 (1-1225)

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Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer  25
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; Publication No. US2004010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1235
; LENGTH: 1225
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US2004010136A1 g189313

US-10-305-720-1235

Alignment Scores:
Pred. No.:   Length: 1225
Score: 6.02e-176   Matches: 319
Percent Similarity: 1678.50   Conservative: 19
Best Local Similarity: 95.48%   Mismatches: 11
Query Match: 90.11%   Indels: 5
DB: 89.90%   Gaps: 1
                            6

US-09-367-052-2 (1-359)   x US-10-305-720-1235 (1-1225)

Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyTyrAspSer   25
              :::||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db   35 ATCAGTATATACACTTCAGATAACTACACCGAGGAAATGGGCTCAGGGGACTATGACTCC   94

Qy   26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr   45
              :::||||||| |||||||:::|||||||||||||||||||||||||||||||||
Db   95 ATGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCACC   154

Qy   46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet   65
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   155 ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG   214

Qy   66 GlyTyrGlnLysGlyLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla   85
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   215 GGTTACCAGAAGGGACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC   274

Qy   86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr   105
              |||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db   275 GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC   334

Qy   106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer   125
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   335 TTTGGGAACTTCCTATGCAAGGCAGTCCATATCATCTACACAGTCAACCTCTACAGCAGT   394

Qy   126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn   145
              |||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db   395 GTCCTCATCCTGGCTTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC   454

Qy   146 SerGlnArgProArgLysLeuLeuAlaGluLysValAlaValTyrValGlyValIlePro   165
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   455 AGTCAGAGGCCCAAGGAAGCTGTTGCTGAAAAGGTGGTCTATGTTGGCGTCATTGGCCCT   514

Qy   166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer   185
              |||||||||||||||||||:::|||||||||||||| ------AGT
Db   515 GCCCTCCTGCTGACTATCCCGACTTTCATCTTTGCCGATGTGTCTCAGGGTGACATTTCA   559

Qy   186 GlnGlyAspAspArgTyrIleCysAspArgLeuTrpProAspSerLeuTrpMetValVal   205
              ::: |||||||||||||||||||||||||||||||||:::||||||||||||||||
Db   560 GAGGCAGATGACAGATATCTGTGACCGTCATTGGGGTGGGTTGTG   619

Qy   206 PheGlnHisIleIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys   225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   620 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC   679

US-10-305-720-1235
; Sequence 1235, Application US/10305720

RESULT 10

RESULT 11
US-10-775-920-370
; Sequence 370, Application US/10775920
; Publication No. US20040175744A1
; GENERAL INFORMATION:
;   APPLICANT: Mergen Ltd
;   TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
;   TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
;   TITLE OF INVENTION: IN CERTAIN CANCERS
;   FILE REFERENCE: Mergen - 0010B
;   CURRENT APPLICATION NUMBER: US/10/775,920
;   CURRENT FILING DATE: 2004-02-10
;   PRIOR APPLICATION NUMBER: US 60/447,900
;   PRIOR FILING DATE: 2003-02-13
;   NUMBER OF SEQ ID NOS: 385
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 370
;   LENGTH: 1225
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-775-920-370

Alignment Scores:

Pred. No.:		Length:	1225
Score:	6.02e-176	Matches:	319
	1678.50	Conservative:	19
Percent Similarity:	95.48%	Mismatches:	11
Best Local Similarity:	90.11%	Indels:	5
Query Match:	89.90%	Gaps:	1
DB:			

US-09-367-052-2 (1-359) x US-10-775-920-370 (1-1225)

```
Qy      6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer      25
            :::||    |||||||||||||||   ||||:::|||||
Db     35 ATCAGTATATACACTTCAGATAACTACACCCGAGAAATGGGCTCAGGGACTATGACTTCC      94

Qy     26 AsnGlyProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr      45
            |||||||||||||||    |||:::||
Db     95 ATGAAGGAACCCTGTTTCCCTGAAGAAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC     154

Qy     46 IleTyrPheIlePheLeuThrGlyIleLeuValGlyLeuValIleLeuValMet      65
            |||||     ||||||||||||||||||||||||||||||||||
Db    155 ATCATCACTCCATCATCTTTCTTAACTGGCATTGTGGGCAATGGCAATGGATTGGTCATCCTGGTCATG     214
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Qy   66 GlyTyrGlnLysLysArgSerMetThrAspTyrTyrArgLeuHisLeuSerValAla   85
Db   215 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAGTACAGCTACAGGCTGCACCTGTCAGTGGCC   274

Qy   86 AspLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr   105
Db   275 GACCTCCTCTTGTCATCACGCTTCCCTTCGGGCAGTGGAGTGATGCCGTGGCAAACTGGTAC   334

Qy   106 PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSer   125
Db   335 TTTGGAAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT   394

Qy   126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn   145
Db   395 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC   454

Qy   146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro   165
Db   455 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT   514

Qy   166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer   185
Db   515 GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAACGTC----------AGT   559

Qy   186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal   205
Db   560 GAGGCAGATGACAGATATATCTGTGACCGGCTTTACCCCCAATGACTTGTGGGTGGTGTG   619

Qy   206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys   225
Db   620 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC   679

Qy   226 TyrCysIleIleLeuSerLysHisSerLysGlyHisGlnLysArgLysAlaLeu   245
Db   680 TATTGCATTATCATCTTCCAAGCTGTCACACTCCAAGGGCCACCAGAGGCGCAAGGCCCTC   739

Qy   246 LysThrThrValIleLeuIleLeuAlaPheAlaCysTrpLeuProTyrTyrValGly   265
Db   740 AAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGCTGCCTTACTACACATTGGG   799

Qy   266 IleSerIleAspSerPheIleLeuLeuGluLeuGlyValIleLeuLysCysAspPheGluSer   285
Db   800 ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC   859

Qy   286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn   305
Db   860 ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTGTCTGAAC   919

Qy   306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerArgAlaGlnHisAlaLeuAsn   325
Db   920 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTGCCCAGCACGCACTCACC   979

Qy   326 SerMetSerArgGlySerSerLeuLysSerLeuLysSerLysLysArgGlyGlyHisSer   345
Db   980 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA   1039

Qy   346 SerValSerThrGluSerSerGluSerSerPheHisSerSer   359
Db   1040 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC   1081

RESULT 12
US-10-785-230-2
; Sequence 2, Application US/10785230
; Publication No. US20040209837A1
; GENERAL INFORMATION:
;   APPLICANT: KISHIMOTO, Tadamitsu
;   APPLICANT: NAGASAWA, Takashi
;   APPLICANT: TACHIBANA, Kazunobu
;   APPLICANT: CHUGAI SEIYAKU KABUSIKI KAISHA
;   TITLE OF INVENTION: Vascularization Inhibitors
;   FILE REFERENCE: 46124-5042-US
;   CURRENT APPLICATION NUMBER: US/10/785,230
;   CURRENT FILING DATE: 2004-02-25

;   PRIOR APPLICATION NUMBER: PCT/JP99/01448
;   PRIOR FILING DATE: 1999-03-23
;   PRIOR APPLICATION NUMBER: JP10/95448
;   PRIOR FILING DATE: 1998-03-24
;   NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
;   LENGTH: 1588
;   TYPE: DNA
;   ORGANISM: Mus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1059)
US-10-785-230-2

Alignment Scores:
Pred. No.:   8.97e-176
Score: 1678.50
Percent Similarity: 95.48%
Best Local Similarity: 90.11%
Query Match: 89.90%
DB: 8

US-09-367-052-2 (1-359) x US-10-785-230-2 (1-1588)

Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
          ::|||||||||||||||||||||||||||:|||||||:::||||||
Db   10 ATCAGTATATACACTTCAGATAACTAACACCGAGGAAATGGGCTCAGGGGACTATGACTCC 69

Qy   26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db   70 ATGAAGGAGAACCCTGTTTCCGTGAGAGAAAATGCTAATTTCAATAAAAATCTTCCTGCCCACC 129

Qy   46 IleTyrPheIleIlePheLeuThrGlyIleLeuValGlyAsnGlyLeuValIleLeuValMet 65
Db 130 ATCTACTTCATCATCTTCTTAACTGGCAATGGCATTGTGGGCAATGGTCATCCTGGTCATG 189

Qy   66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 190 GGTTACCAGAAGAAACTGAGAAGCATGACCGACAAGTACAGGCTGCACCTGTCAGTGGCC 249

Qy   86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
Db 250 GACCTCCTTTTCGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCATGGCAAACTGGTAC 309

Qy 106 PheGlyLysPheLeuCysLysPheLeuAsnAlaValHisIleLeuTyrThrValAsnLeuTyrSerSer 125
Db 310 TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCCATCTACCACAGTCAACCTCTACAGCAGT 369

Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
Db 370 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC 429

Qy 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
Db 430 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT 489

Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheLeuAlaAspValSerGlnGlyAspIleSer 185
Db 490 GCCCTCCTGCTGACTATTCCCGACTTCATCTTTCTGGCAGATGTC------------AGT 534

Qy 186 GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
Db 535 GAGGCAGATGACAGATATCCGTGACCCCTTCTACCCCAATGACTTGTGGGTGGTTGTG 594

Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
Db 595 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC 654

Qy 226 TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
Db 655 TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 714

Qy 246 LysThrThrValIleLeuLeuIleLeuLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265

RESULT 13
US-10-775-920-372
; Sequence 372, Application US/10775920
; Publication No. US20040175744A1
; GENERAL INFORMATION:
;   APPLICANT: Mergen Ltd
;   TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
;   TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
;   TITLE OF INVENTION: IN CERTAIN CANCERS
;   FILE REFERENCE: Mergen - 0010B
;   CURRENT APPLICATION NUMBER: US/10/775,920
;   CURRENT FILING DATE: 2004-02-10
;   PRIOR APPLICATION NUMBER: US 60/447,900
;   PRIOR FILING DATE: 2003-02-13
;   NUMBER OF SEQ ID NOS: 385
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 372
;   LENGTH: 1637
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-775-920-372

Alignment Scores:
Pred. No.:   9.4e-176
Score: 1678.50
Percent Similarity: 95.48%
Best Local Similarity: 90.11%
Query Match: 89.90%
DB: 8

US-09-367-052-2 (1-359) x US-10-775-920-372 (1-1637)

Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer 25
Db   94 ATCAGTATATACACTTCAGATAACTAACACCGAGGAAATGGGCTCAGGGGACTATGACTCC 153

Qy   26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
Db 154 ATGAAGGAGAACCCTGTTTCCGTGAGAGAAAATGCTAATTTCAATAAAAATCTTCCTGCCCACC 213

Qy   46 IleTyrPheIleIlePheLeuThrGlyIleLeuValGlyAsnGlyLeuValIleLeuValMet 65
Db 214 ATCTACTTCATCATCTTCTTAACTGGCAATGGCATTGTGGGCAATGGTCATCCTGGTCATG 273

Qy   66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
Db 274 GGTTACCAGAAGAAACTGAGAAGCATGACCGACAAGTACAGGCTGCACCTGTCAGTGGCC 333

Qy   86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105

Db 715 AAGACCAGCCAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGCTGCCTACTACATTGGG 774

Qy 266 IleSerIleAspSerPheIleLeuLeuGlyValIleLeuGlyGlyLysCysAspPheGluSer 285
Db 775 ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 834

Qy 286 IleValHisLysTrpIleSerIleThrGluAlaPheHisCysCysLeuAsn 305
Db 835 ACTGTGCACAGTGATGATTTCCATCACCGAGGCCTTTCTTCCACTGTGTCTGAAC 894

Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
Db 895 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC 954

Qy 326 SerMetSerArgGlySerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
Db 955 TCTGTGAGCAGAGGGTCCAGCCTCAGAATCCTCTCCAAGAGCAAAGGAAAGCGAGGTGGACATTCA 1014

Qy 346 SerValSerThrGluSerSerSerPheHisSerSer 359
Db 1015 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC 1056

```
;  ORGANISM: Homo sapiens
US-10-775-920-374

Alignment Scores:
Pred. No.:                      Length:          1645
Score:             9.47e-176    Matches:         319
Percent Similarity:  1678.50    Conservative:    19
Best Local Similarity: 95.48%   Mismatches:      11
Query Match:          90.11%    Indels:          5
                      89.90%    Gaps:            1
DB:                   8

US-09-367-052-2 (1-359)  x  US-10-775-920-374  (1-1645)

Qy      6  ValSerIleTyrThrSerAspAsnTyrSerGluGluValGlySerGlyAspTyrAspSer   25
           ::::|||||:::||||||||||||||::||||:::::||||||:::||||||||||||||||
Db     77  ATCAGTATATACACTTCAGATAACTAACACACCGAGAAATGGCTCAGGGGACTATGACTCC  136

Qy     26  AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr   45
           |||||||||||||||||:::|||:::  ::|||||||||  :::::|||||||||||||||||
Db    137  ATGAGGAACCCCTGTTCCGTGAAGAAAATGCTAATTCAATAAAAATCTTCCTGCCCACC  196

Qy     46  IleTyrPhelleLeuPheLeuThrGlyTyrIleValGlyLeuValIleLeuValMet   65
           ||||||||||||||||||||||:::||:::|||||||||||||||||||||||||||||
Db    197  ATCTACTCACCATCTTCTTAACTGGCATTGTGGGCAATGGATTGTCATCCTGGTCATG  256

Qy     66  GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla   85
           :::||||||||||||:::|||:::|||||||||||||||||||||||||||||||||||||
Db    257  GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC  316

Qy     86  AspLeuPheValIleThrLeuProPheThrValProPheTrpAlaValAlaAspTrpTyr  105
           |||||||||||||||||||||||||:::||||||||||||:::|||||||||||||||||
Db    317  GACCTCTTCGTCATCACGCTTCCCTTCCTGTCGCCAGTGCCAGTGGCAAACTGGTAC   376

Qy    106  PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
           ||||||||||||:::||:::||||||||||||||||||||||||||||||||||||||||
Db    377  TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCACAGCAGT  436

Qy    126  ValLeulleLeuAlaPhelleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
           ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db    437  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTCACCTGGCCATCGTCCACGCCACCAAC  496

Qy    146  SerGlnArgProArgLysLeuLeuAlaGluLysAlaValAlaValTyrValGlyValTrpIlePro  165
           |||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db    497  AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT  556

Qy    166  AlaLeuLeuLeuThrIleProAspPhelleProPheAlaAspValSerGlnGlyAspIleSer  185
           ::::::::::::::|||||:::::||||||||||||||||||||||||||||::::------AGT  601
Db    557  GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAACGTC--------------

Qy    186  AlaLeuLeuThrIleMetValGlyLeuLeuProGlyIleLeuLeuSerCys  205
           :::  |||||||||||||||||||||||||:::||||||||||||||||||||
Db    602  GAGGCAGATGACAGATATATCGTGACCGGCTTCTACCCCAATGACTTGTGGGTGGTTGTG  661

Qy    206  PheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleLeuLeuSerCys  225
           :::|||||||||||||||||||||||||||||:::|||||||||||||||||||
Db    662  TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGGTATTGTCATCCTGTCCTGC  721

Qy    226  TyrCysIleIleSerLysSerHisSerLysGlyHisGlnLysArgLysAlaLeu  245
           |||||||:::::||||||||||||||||||||||||||||||||||||||||||
Db    722  TATTGCATTATCATCTCCAAGTCTGTCACACTCCAAGGGCCACCAGAAGGGCAAGAGGCCCTC  781

Qy    246  LysThrThrValLeulleLeuLeuVallleLeuProTyrTyrValGly  265
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    782  AAGACCACAGTCATCCTCATCCTGCTTTTCTTCCTGCCTGTTACTATTGGG  841

Qy    266  IleSerIleAspSerPhelleLeuGlyValIleLysGlyCysAspPheGluSer  285
           :::::||||||||||||||||||||||||||||||:::||||||||||||||||
Db    842  ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC  901

Qy    286  IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysTyrLeuAsn  305
           ||||||:::|||||||||||||:::||||||||||||||||||||||||||||||||||
Db    902  ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC  961
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Db    334  GACCTCCTCTTGTCATCACGCTTCCCTTCTGGGCAGTGATGCCGTGGCAAACTGGTAC  393
Qy    106  PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
           ||||||  |||||||:::|||||||||||||||||||||||||||||||||||||||||
Db    394  TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCACAGCAGT  453

Qy    126  ValLeulleLeuAlaPhelleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
           ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||||
Db    454  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTCACCTGGCCATCGTCCACGCCACCAAC  513

Qy    146  SerGlnArgProArgLysLeuLeuAlaGluLysAlaValAlaValTyrValGlyValTrpIlePro  165
           |||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db    514  AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT  573

Qy    166  AlaLeuLeuLeuThrIleProAspPhelleProPheAlaAspValSerGlnGlyAspIleSer  185
           ::::::::::::::|||||:::::||||||||||||||||||||::::------AGT
Db    574  GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCC--------------AGT  618

Qy    186  GlnGlyAspAspArgTyrIleCysAspAspArgTyrTrpMetValVal  205
           :::  |||||||||||||||||||||:::||||||||||||||||||||
Db    619  GAGGCAGATGACAGATATATCGTGACCGGCTTGTGGGTTGTG  678

Qy    206  PheGlnPheGlnHisIleMetValGlyLeuLeuProGlyIleLeuVallleLeuSerCys  225
           |||||||||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db    679  TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGGTATTGTCATCCTGTCCTGC  738

Qy    226  TyrCysIleIleSerLysSerHisSerLysGlyHisGlnLysArgLysAlaLeu  245
           |||||||:::::||||||||||||||||||||||||||||||||||||||||||
Db    739  TATTGCATTATCATCTCCAAGTCTGTCACACTCCAAGGGCCACCAGAAGGGCAAGAGGCCCTC  798

Qy    246  LysThrThrValLeulleLeuLeuVallleLeuProTyrTyrValGly  265
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    799  AAGACCACAGTCATCCTCATCCTGCTTTTCTTCCTGCCTGTTACTATTGGG  858

Qy    266  IleSerIleAspSerPhelleLeuGlyValIleLysGlyCysAspPheGluSer  285
           :::::||||||||||||||||||||||  :::|||||||||||||||||||||||
Db    859  ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC  918

Qy    286  IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysTyrLeuAsn  305
           ||||||:::|||||||||||||:::||||||||||||||||||||||||||||||||||
Db    919  ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC  978

Qy    306  ProIleLeuTyrAlaPheLeuGlyTyrAlaLysPheSerSerAlaGlnHisAlaLeuAsn  325
           :::|||||||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db    979  CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC  1038

Qy    326  SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyGlyArgGlyGlyHisSer  345
           :::|||||||||||||||||||||||||||||||||||||||||||||||||||:::---AGT
Db    1039  TCTGTGAGCAGAGGGTCCAGCCTCCAAGATCCTCCAAGAGGAAAGCGAGGTGGACATTCA  1098

Qy    346  SerValSerThrGluSerGluSerProPheHisSerSer  359
           ||||||||||||||||||||||||||||||||||||||||
Db    1099  TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTCACTCCAGC  1140
```

RESULT 14
US-10-775-920-374

; Sequence 374, Application US/10775920
; Publication No. US20040175744A1
; GENERAL INFORMATION:
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Mergen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 374
; LENGTH: 1645
; TYPE: DNA

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Qy   306  ProIleLeuTyrAlaPheLeuGlyPheLysSerSerAlaGlnHisAlaLeuAsn  325
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   962  CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC  1021

Qy   326  SerMetSerArgGlySerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer  345
          ||||:::||||||||||||||||||||||||||||||||||||||||||||
Db   1022 TCTGTGAGAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA  1081

Qy   346  SerValSerThrGluSerSerSerPheHisSerSer  359
          ||||||||||||||||||||||||||||||||||
Db   1082 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC  1123


RESULT 15
US-10-505-680-185
; Sequence 185, Application US/10505680
; Publication No. US20050095592A1
; GENERAL INFORMATION:
;  APPLICANT: The Government of the United States of America as represented by the
;  APPLICANT: Secretary of the Department of Health and Human Services
;  APPLICANT: Jazaeri, Amir A.
;  APPLICANT: Boyd, Jeff
;  APPLICANT: Liu, Edison T.
;  TITLE OF INVENTION: IDENTIFICATION OF OVARIAN CANCER TUMOR MARKERS AND THERAPEUTIC TA
;  FILE REFERENCE: 4239-64452
;  CURRENT APPLICATION NUMBER: US/10/505,680
;  CURRENT FILING DATE:  2004-08-12
;  PRIOR APPLICATION NUMBER: 60/357,031
;  PRIOR FILING DATE: 2002-02-13
;  NUMBER OF SEQ ID NOS: 822
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 185
;  LENGTH: 1645
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-505-680-185

Alignment Scores:
Pred. No.:             9.47e-176      Length:         1645
Score:                 1678.50        Matches:        319
Percent Similarity:    95.48%         Conservative:   19
Best Local Similarity: 90.11%         Mismatches:     11
Query Match:           89.90%         Indels:         5
DB:                    9              Gaps:           1

US-09-367-052-2 (1-359) x US-10-505-680-185  (1-1645)

Qy     6  ValSerIleTyrThrSerAspAsnTyrSerGlyGluValGlySerGlyAspTyrAspSer  25
          ::|||||||||||||||||||||||||:::||||||:::|||||||||||||
Db    77  ATCAGTATATACACTTCAGATAACTACACACCGAGGAAATGGCTCAGGGGACTATGACTTC  136

Qy    26  AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr  45
          |||||||||||||:::||||:::||||||||||||||||||:::|||||||||||
Db   137  ATGAAGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC  196

Qy    46  IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet  65
          |||||||||||||||||:::|||||||||||||||||||||||||||||
Db   197  ATCTACTTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG  256

Qy    66  GlyTyrGlnLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla  85
          |||||||||||||||||||||||||||||||||||||||||||||
Db   257  GGTTACCAGAAGAAAACTGAGAAGTACAGGCTGCACCTGTCAGTGGCC  316

Qy    86  AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr  105
          |||||||||||||||||||||||||||:::||||||||||||||||
Db   317  GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC  376

Qy   106  PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
          |||||||||||||||||||:::||||||||||||||||||||||||||||||
Db   377  TTTGGGAAACTTCCATGCAAGGCAGTCCATATCCATCTACACAGTGAACCTCTACAGCAGT  436

Qy   126  ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   437  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC  496
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Qy   146  SerGlnArgProArgLysLeuLeuAlaGlnAlaValTyrValGlyValTrpIlePro  165
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   497  AGTCAGAGGCCAAGGAAGCTGTTGGCTCAAGCAGTGGTCTATGTGGGCGTCTGGATCCCT  556

Qy   166  AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer  185
          ||||||||||||||||||||||||||||||||||::::||
Db   557  GCCCTCCTGCTCGACTATTCCCGACTTCATCTTTGCCAACGTC----------AGT  601

Qy   186  GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal  205
          :::              |||:::            :::|||
Db   602  GAGGCAGATGACAGATATATCTGTGACCGGCTTTACCCCAATGACTTGTGGGTGGTTGTG  661

Qy   206  PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys  225
          |||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db   662  TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC  721

Qy   226  TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu  245
          |||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   266  IleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCysAspPheGluSer  285
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Qy   306  ProIleLeuTyrAlaPheLeuGlyPheLysSerSerAlaGlnHisAlaLeuAsn  325
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Qy   326  SerMetSerArgGlySerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer  345
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Search completed: January 11, 2006, 02:44:21
Job time : 1051 secs

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                    GenCore version 5.1.6
            Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    January 11, 2006, 00:27:42 ; Search time 257 Seconds
                                (without alignments)
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Title:          US-09-367-052-2
Perfect score:  1867
Sequence:       1 MEPISVSIYTSDNYSEEVGS........KRGGHSSVSTESESSSPHSS 359

Scoring table:  BLOSUM62
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Searched:       437633 seqs, 36453575 residues

Total number of hits satisfying chosen parameters:        9275266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match  0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	1744.5	93.4	1050	7	US-11-028-922A-4	Sequence 4, Appli
2	1738.5	93.1	1651	7	US-11-136-527-2630	Sequence 2630, Ap
3	1678.5	89.9	1225	6	US-10-955-054A-112	Sequence 112, App
4	1678.5	89.9	1662	7	US-11-028-922A-3	Sequence 3, Appli
5	1672.5	89.6	8747	6	US-10-955-054A-141	Sequence 141, App
6	1670.5	89.5	1102	6	US-10-955-054A-121	Sequence 121, App
7	1606	86.0	1643	7	US-11-136-527-108	Sequence 108, App
8	1320.5	70.7	1400	7	US-11-136-527-6726	Sequence 6726, Ap

9	1268	67.9	1400	7	US-11-136-527-4204	Sequence 4204, Ap
10	594	31.8	1680	7	US-11-136-527-153	Sequence 153, App
11	576	30.9	1400	7	US-11-136-527-4249	Sequence 4249, Ap
12	562	30.1	1324	7	US-11-136-527-2373	Sequence 2373, Ap
13	540	28.9	3100	6	US-10-775-169-254	Sequence 254, Appl
14	535	28.7	3177	6	US-11-127-877-25	Sequence 25, Appl
15	533	28.5	30151	6	US-10-995-561-13239	Sequence 13239, A
16	531	28.4	3062	6	US-10-995-561-120	Sequence 120, App
17	531	28.4	3101	6	US-10-995-561-119	Sequence 119, App
18	522.5	28.0	246960	7	US-11-121-086-8	Sequence 8, Appli
19	510.5	27.3	1348	6	US-11-136-527-3311	Sequence 3311, Ap
20 c	508	27.2	1433	6	US-10-750-185-54253	Sequence 54253, A
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22	498	26.7	2273	7	US-11-127-877-23	Sequence 23, Appl
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24	493.5	26.4	1251	7	US-11-122-849-1	Sequence 1, Appli
25	492.5	26.4	1383	7	US-11-136-527-3271	Sequence 3271, Ap
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28	483.5	25.9	3655	7	US-11-127-877-24	Sequence 24, Appl
29	477.5	25.6	1915	7	US-11-068-686-3	Sequence 3, Appli
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33	463.5	24.8	2214	6	US-10-995-561-196	Sequence 196, App
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39	463.5	24.8	57198	6	US-10-995-561-13263	Sequence 13263, A
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43	460.5	24.7	2156	7	US-11-136-527-3843	Sequence 3843, Ap
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ALIGNMENTS

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; Sequence 4, Application US/11028922A
; Publication No. US2005027163A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Marc
;  TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
;  FILE REFERENCE: CCF-7019
;  CURRENT APPLICATION NUMBER: US/11/028,922A
;  CURRENT FILING DATE: 2005-01-04
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
;  LENGTH: 1050
;  TYPE: DNA
;  ORGANISM: Rattus norvegicus
US-11-028-922A-4

  Alignment Scores:
  Pred. No.:              2.97e-189     Length:              1050
  Score:                    1744.50     Matches:              338
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  Best Local Similarity:     95.48%     Mismatches:             7
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APPLICANT: Wyeth
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2630
LENGTH: 1651
TYPE: DNA
ORGANISM: Rattus norvegicus
US-11-136-527-2630

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Pred. No.:              2.8e-188        Length:         1651
Score:                  1738.50         Matches:        337
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US-09-367-052-2 (1-359) x US-11-136-527-2630 (1-1651)

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Qy  306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
        ||||||||||||||||||||::||||||||||||||::|||||
Db  920 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCGCCCAGCACGCACTCACC 979

Qy  326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysHisSer 345
        |||::::|||||||||||||||||||||::|||||||||||||
Db  980 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGGTGGACATTCA 1039

Qy  346 SerValSerThrGluSerSerSerPheHisSerSer 359
        |||||||||||||||||||||||||||||||
Db 1040 TCTGTTTCCACTGAGTCTGAGTCTTCAGTTTTCACTCCAGC 1081
```

RESULT 4
US-11-028-922A-3
; Sequence 3, Application US/11028922A
; Publication No. US2005027139A1
; GENERAL INFORMATION:
;   APPLICANT: Penn, Marc
;   TITLE OF INVENTION: GENETICALLY ENGINEERED FOR THERAPEUTIC APPLICATIONS
;   FILE REFERENCE: CCF-7019
;   CURRENT APPLICATION NUMBER: US/11/028,922A
;   CURRENT FILING DATE: 2005-01-04
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-028-922A-3

```
Qy  246 LysThrThrValIleLeuIleLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db  706 AAGACTACGGTCATCCTATCCTGGCTTTCTTTGCCTGCTGGCTACCGTATTACGTGGGG 765

Qy  266 IleSerIleAspSerPheIleLeuLeuGluGlyValIleLysGlnGlyGlyCysAspPheGluSer 285
        ||||||||||||||||||||||||||||||||||::|||||||
Db  766 ATCAGCATCGATTCCTTCATCCTTCTTGGAGGATGTCATCAAGCAAGGATGTGAGTTCGAGAGC 825

Qy  286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
        ||||||||||||||||||||||||||||||||||||||||||||
Db  826 GTCGTGCACAAGTGGATCTCCATCACGGAGGCCCTCGCCTTCTTCCACTGTTGCCTGAAC 885

Qy  306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
        ||||||||||||||||||||||||||||||||||||||||||||
Db  886 CCCATCCTCTACGCCTTCCTGGGGGCCAAATTCAAGAGCTCCGCGCAGCATGCACTCAAT 945

Qy  326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyLysHisSer 345
        ||||||||||||||||||||||||||||||||||||||||||||
Db  946 TCCATGAGCAGAGGCTCCAGCCTCAAGATCCTTTCCAAAGGAAACGGGGGTGGACACTCT 1005

Qy  346 SerValSerThrGluSerSerSerPheHisSerSer 359
        |||||||||||||||||||||||||||||||
Db 1006 TCCGTCTCCACAGAGTCAGAATCCTCAAGTTTTCACTCCAGC 1047
```

RESULT 3
US-10-955-054A-112
; Sequence 112, Application US/10955054A
; GENERAL INFORMATION:
;   Publication No. US2005026420A1
;   APPLICANT: PUSZTAI, LAJOS
;   APPLICANT: SYMMANS, W. FRASER
;   APPLICANT: HESS, KENNETH R.
;   APPLICANT: AYERS, MARK
;   APPLICANT: STEC, JAMES
;   TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
;   FILE REFERENCE: UTXC:880US
;   CURRENT APPLICATION NUMBER: US/10/955,054A
;   CURRENT FILING DATE: 2004-09-30
;   NUMBER OF SEQ ID NOS: 195
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
;   LENGTH: 1225
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-955-054A-112

Alignment Scores:
Pred. No.:   1.32e-181   Length: 1225
Score: 1678.50   Matches: 319
Percent Similarity: 95.48%   Conservative: 19
Best Local Similarity: 90.11%   Mismatches: 11
Query Match: 89.90%   Indels: 5
DB: 6   Gaps: 1

US-09-367-052-2 (1-359) x US-10-955-054A-112 (1-1225)

```
Qy    6 ValSerIlePheTyrThrSerAspAsnTyrSerGluGluValGlyValGlySerGlyTyrAspSer 25
        :::||||||||||||||||||||||::|||||||||::|||||
Db   35 ATCAGTATATACACTTCAGATAATACACCGAGGAAATGGCCTCAGGGGACTATGACTCC 94

Qy   26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
        |||||||||||||||||    :::||||||||||||||||||||||
Db   95 ATGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC 154

Qy   46 IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMet 65
        ||||||||||||||||||||||||||||||||||||||||||||
Db  155 ATCTACTTCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 214

Qy   66 GlyTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla 85
        ||||||||||||||||||||||||||||||||||||||||||||
Db  215 GGTTACCAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC 274
```

```
Alignment Scores:
Pred. No.:              2.07e-181          Length:              1662
Score:                  1678.50            Matches:             319
Percent Similarity:     95.48%             Conservative:        19
Best Local Similarity:  90.11%             Mismatches:          11
Query Match:            89.90%             Indels:              5
DB:                                        Gaps:                1
```

US-09-367-052-2 (1-359) x US-11-028-922A-3 (1-1662)

```
Qy      6  ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer  25
           :::||||:|||||||||||||||||||:||||||||||||||||||||||||||||||
Db     63  ATCAGTATATACACTTCAGATAACTACACCGAGGGAAATGGGCTCAGGGGACTATGACTCC  122

Qy     26  AsnLysGluProCysPheArgGluAspAlaAsnValHisPheAsnArgIlePheLeuProThr  45
           :: ||||||:||||||||||||||||:||:||||||||||:||||||||||:||||||
Db    123  ATGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC  182

Qy     46  IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleIleLeuValMet  65
           ||||||||||:||:||:|||:||||||||||||||||:|||||||||||||||||||||
Db    183  ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG  242

Qy     66  GlyTyrTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla  85
           |||||||||:||||||||||||||||||:|||||||||||||||||||||||||||:|:
Db    243  GGTTACCCAGAAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC  302

Qy     86  AspLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpIleTyr  105
           ::|||||||:||||||||||||||||:|||||||||||:|||:||:||||||||||||
Db    303  GACCTCCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGCAAACTGGTAC  362

Qy    106  PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
           |||||||||||:||||:||||||:::|||||||||||:||:||||||||||||||||||
Db    363  TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT  422

Qy    126  ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
           ||||||||:|||||||||||:||||||||||||||||||||||||||||:|||||||
Db    423  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC  482

Qy    146  SerGlnArgProArgLysLeuAlaGluLysArgValGlyValTrpIlePro  165
           |||||||||||:|||||||||||||||||||:|||:|||||||||||||||
Db    483  AGTCAGAGGCCAAGGAAGCTGGCTGAAAAGCGGGTCTATGTTTGGCGTTCTGGATCCCT  542

Qy    166  AlaLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer  185
           ||||:||||||:|||||||||||||:||:||||||||||||||||||||-------AGT
Db    543  GCCCTCCTGCTATTCCCGACTTCATCTTTGCCAAGTC                587

Qy    186  GlnGlyAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal  205
           :::  |||:|:|:|:||:|||||||||||||||||:|||:||||:|||||:||||||||
Db    588  GAGGCAGATGACAGATATATCTGTGACCGGCTTCTACCCCAATGACTTGTGGGGTGGTGTG  647

Qy    206  PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys  225
           ||||||||||||:||||||||||||||||||||||||||:||||||||||||||||||
Db    648  TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC  707

Qy    226  TyrCysIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu  245
           |||:|:||:||:|||||||||||||||||||||||||||||||||||||||||||||||
Db    708  TATTGCATTATCATCTCCAAGCTGTCACACTCCAAGGGCCACCAGAAGAGGAAGGCCCTC  767

Qy    246  LysThrThrValIleLeuIleLeuLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly  265
           ||||||||:||||||||||:|||:|||||:|||||||||||||||:|||||||||||||||
Db    768  AAGACCACAGTCATCCTCATCCTGGCTTTCTTTGCCTGCTGGCTCCCTTACTACGTTGGG  827

Qy    266  IleSerIleAspSerPheIleLeuLeuGluIleIleLysGlnGlyCysAspPheGluSer  285
           ||:||:||||||||:|||||:|||:||||||||||||||||||||:|||:|:  |||:::
Db    828  ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC  887

Qy    286  IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn  305
           ||:||||||:||||||||||:||:||||||||||:||:||||||||:|||:|||:||||
Db    888  ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTTGCTTTCTTCCACTGTTGTCTGAAC  947

Qy    306  ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn  325
           ||||||||||||||:|||||||||||:||:||||||||||||:|||:||||||||||||
Db    948  CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCGCACTCACC  1007

Qy    326  SerMetSerArgGlySerSerArgLeuIleLeuSerLysGlySerGlyArgGlyGlyHisSer  345
           |||:|||||||||||||||||:||||||||:|||||||||||||||||||||||||||||
Db   1008  TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA  1067

Qy    346  SerValSerThrGluSerGluSerSerPheHisSerSer  359
           |||||||||||||||||||||:||||||:|||||||||||
Db   1068  TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC  1109
```

```
RESULT 5
US-10-955-054A-141
; Sequence 141, Application US/10955054A
; Publication No. US2005026642 0A1
; GENERAL INFORMATION:
;   APPLICANT:  PUSZTAI, LAJOS
;   APPLICANT:  SYMMANS, W. FRASER
;   APPLICANT:  HESS, KENNETH R.
;   APPLICANT:  AYERS, MARK
;   APPLICANT:  STEC, JAMES
;   TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
;   FILE REFERENCE: UTXC:880US
;   CURRENT APPLICATION NUMBER: US/10/955,054A
;   CURRENT FILING DATE: 2004-09-30
;   NUMBER OF SEQ ID NOS: 195
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
;   LENGTH: 8747
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-955-054A-141
```

```
Alignment Scores:
Pred. No.:                                 Length:              8747
Score:                  1.15e-179          Matches:             318
Percent Similarity:     95.20%             Conservative:        19
Best Local Similarity:  89.83%             Mismatches:          12
Query Match:            89.58%             Indels:              5
DB:                                        Gaps:                1
```

US-09-367-052-2 (1-359) x US-10-955-054A-141 (1-8747)

```
Qy      6  ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer  25
           :::||||:||||||||||||||||||:|||||||||||||||||||||||||||:
Db   4862  TTGCAGATATACACTTCAGATAACTACACCGAGGGAAATGGGCTCAGGGGACTATGACTCC  4921

Qy     26  AsnLysGluProCysPheArgGluAspAlaAsnValHisPheAsnArgIlePheLeuProThr  45
           :: ||||||:||||||||||||||||:||:||||||||||:||||||||||:||||||
Db   4922  ATGAAGGAACCCTGTTTCCGTGAAGAAAATGCTAATTTCAATAAAATCTTCCTGCCCACC  4981

Qy     46  IleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleIleLeuValMet  65
           ||||||||||:||:||:|||:||||||||||||||||:|||||||||||||||||||||
Db   4982  ATCTACTCCATCATCTTCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG  5041

Qy     66  GlyTyrTyrGlnLysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAla  85
           |||||||||:||||||||||||||||||:|||||||||||||||||||||||||||:|:
Db   5042  GGTTACCCAGAAGAAGAAACTGAGAAGCATGACGGACAAGTACAGGCTGCACCTGTCAGTGGCC  5101

Qy     86  AspLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpIleTyr  105
           ::|||||||:||||||||||||||||:|||||||||||:|||:||:||||||||||||
Db   5102  GACCTCCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGCAAACTGGTAC  5161

Qy    106  PheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSer  125
           |||||||||||:||||:||||||:::|||||||||||:||:||||||||||||||||||
Db   5162  TTTGGGAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT  5221

Qy    126  ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn  145
           ||||||||:|||||||||||:||||||||||||||||||||||||||||:|||||||
Db   5222  GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATCGTCCACGCCACCAAC  5281

Qy    146  SerGlnArgProArgLysLeuAlaGluLysArgValGlyValTrpIlePro  165
           |||||||||||:|||||||||||||||||||:|||:|||||||||||||||
Db   5282  AGTCAGAGGCCAAGGAAGCTGGCTGAAAAGCGGGTCTATGTTTGGCGTTCTGGATCCCT  5341
```

Qy   6 ValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyrAspSer 25
            :::||||||||||||||||||||||||||||||::::|||||||||||||:::
Db   53 ATCAGATATACACTTCAGATAACTACACCAGGAAATGGCTCAGGGGACTATGACTCC 112

Qy   26 AsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThr 45
            ||||||||:::|||:::|||||||||||||::||
Db 113 ATGAAGGAACCCTGTTTCCGTGACGAAAAATGCTAATTTCAATAAAATCTTCCTGCCACC 172

Qy   46 IleTyrPheIleLeuPheLeuThrGlyIleIleGlyAsnGlyLeuValIleLeuValMet 65
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 173 ATCTACTTCCATCATCTTCCTTAACTGGCATTGTGGGCAATGGATTGGTCATCCTGGTCATG 232

Qy   66 GlyTyrGlnLysLysLeuArgSerMetThrAspIleTyrLeuLeuAsnLeuSerValAla 85
            |||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db 233 GGTTACCAGAAGAAACTGAGGAGCATGACGGACATACAGCTGCTCAACCTGTCAGTGGCC 292

Qy   86 AspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyr 105
            |||||||||||||||||||||||||||||||||||::::||||||||
Db 293 GACCTCCTCTTTGTCATCACGCTTCCCTTCTGGGCAGTTGATGCCGTGGCAAACTGGTAC 352

Qy 106 PheGlyLysPheLeuCysLysValAlaValHisIleIleTyrThrValAsnLeuTyrSer 125
            |||||||||||::||||||||||:::||||||||||||||||||||||||||||
Db 353 TTTGGAAACTTCCTATGCAAGGCAGTCCATGTCATCTACACAGTCAACCTCTACAGCAGT 412

Qy 126 ValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsn 145
            |||||||||||||||||||||||||||::||||||||||||||
Db 413 GTCCTCATCCTGGCCTTCATCAGTCTGGACCGCTACCTGGCCATTGTCCACGCCACCAAC 472

Qy 146 SerGlnArgProArgLysLeuLeuAlaGluLysAlaValTyrValGlyValTrpIlePro 165
            |||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db 473 AGTCAGAGGCCAAGGAAGCTGTTGGCTGAAAAGGTGGTCTATGTTGGCGTCTGGATCCCT 532

Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
            ||||||||||||||||||::||||||||||||||||||::::::   AGT 577
Db 533 GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAAGTC----------AGT 577

Qy 186 GlnIleAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
            :::||||||||||||||||::::::|||||||||||::::
Db 578 GAGGCAGATGACAGATATATCTGTGACCGGCTTTACCCCAATGACTGTGGGTGGGTGTG 637

Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
            ||||||||||||||||||||||||||||||||||||||||||||||
Db 638 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC 697

Qy 226 TyrCysIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 698 TATTGCATTATCATCTCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGAAGGAAGGCCCTC 757

Qy 246 LysThrThrValIleLeuLeuLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
            |||||||::|||||||||||||||||||||||||||||||||||||::::|||
Db 758 AAGACCACAATCATCCCCATCTGCTTTCCTTCGCCGTGTTGGCTGCCTTACTACATTGGG 817

Qy 266 IleSerIleAspSerPheIleLeuLeuGluValIleLysGlnGlyCysAspPheGluSer 285
            ||||||:::|||||||||||||||||||||||||:::|||||||||||||||
Db 818 ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGAGTTTGAGAAC 877

Qy 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
            ||||||||:|||::::::||||||||||||||||||||||||||||||||||||
Db 878 ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTGGCTTTCTTCCACTGTTGTCTGAAC 937

Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
            :::|||||||||||||||||||::::::|||||||||||||::||||||||||
Db 938 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCCACC 997

Qy 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
            ||:::::|||||||||||||||||||||:::||||||||||||||||||||
Db 998 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA 1057

Qy 346 SerValSerThrGluSerSerPheHisSerSer 359
            |||||||||||||||||||||||||||||||
Db 1058 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC 1099

RESULT 7

Qy 166 AlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAspIleSer 185
            ||||||||||||||||||::||||||||||||||||::::::   AGT
Db 5342 GCCCTCCTGCTGACTATTCCCGACTTCATCTTTGCCAACGTC----------AGT 5386

Qy 186 GlnIleAspAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValVal 205
            :::|||||||||||||||||::||||||||||||||:::::
Db 5387 GAGGCAGATGACAGATATATCTGTGACCGGCTTTACCCCAATGACTGTGGGTGGGTTGTG 5446

Qy 206 PheGlnPheGlnHisIleMetValGlyLeuIleLeuProGlyIleValIleLeuSerCys 225
            ||||||||||||||||||||||||||||||||||||::|||
Db 5447 TTCCAGTTTCAGCACATCATGGTTGGCCTTATCCTGCCTGGTATTGTCATCCTGTCCTGC 5506

Qy 226 TyrCysIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAlaLeu 245
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5507 TATTGCATTATCATCTCAAGCTGTCACACTCCAAGGGCCACCAGAAGCGCAAGGCCCTC 5566

Qy 246 LysThrThrValIleLeuLeuLeuAlaPhePheAlaCysTrpLeuProTyrTyrValGly 265
            :::||||||||||||||||||||||||||||||||||||:::|||
Db 5567 AAGACCACAGTCATCCTCATCCTGGCTTTCTTCGCCTGTTGGCTGCCCTACTACATTGGG 5626

Qy 266 IleSerIleAspSerPheIleLeuLeuGluValIleLysGlnGlyCysAspPheGluSer 285
            :::|||||||||||||||||||||||||:::||||||||||
Db 5627 ATCAGCATCGACTCCTTCATCCTCCTGGAAATCATCAAGCAAGGGTGTGAGTTTGAGAAC 5686

Qy 286 IleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeuAsn 305
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5687 ACTGTGCACAAGTGGATTTCCATCACCGAGGCCCTAGCTTTCTTCCACTGTTGTCTGAAC 5746

Qy 306 ProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsn 325
            :::|||||||||||||||||::::||||||||||||||||||:::
Db 5747 CCCATCCTCTATGCTTTCCTTGGAGCCAAATTTAAAACCTCTGCCCAGCACGCACTCACC 5806

Qy 326 SerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSer 345
            ||:::::|||||||||||||||||||||:::||||||||||||||||||::
Db 5807 TCTGTGAGCAGAGGGTCCAGCCTCAAGATCCTCTCCAAAGGAAAGCGAGGTGGACATTCA 5866

Qy 346 SerValSerThrGluSerSerPheHisSerSer 359
            |||||||||||||||||||||||||||||||
Db 5867 TCTGTTTCCACTGAGTCTGAGTCTTCAAGTTTTCACTCCAGC 5908

RESULT 6
US-10-955-054A-121
; Sequence 121, Application US/10955054A
; Publication No. US20050266420A1
; GENERAL INFORMATION:
; APPLICANT: PUSZTAI, LAJOS
; APPLICANT: SYMMANS, W. FRASER
; APPLICANT: HESS, KENNETH R.
; APPLICANT: AYERS, MARK
; APPLICANT: STEC, JAMES
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: UTKC:880US
; CURRENT APPLICATION NUMBER: US/10/955,054A
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 121
; LENGTH: 1102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-955-054A-121

Alignment Scores:
Pred. No.:   1102
Score: 9.32e-181   Length: 1102
Percent Similarity: 1670.50   Matches: 317
Best Local Similarity: 95.20%   Conservative: 20
Query Match: 89.55%   Mismatches: 12
DB: 89.48%   Indels: 5
                        6   Gaps: 1

US-09-367-052-2 (1-359) x US-10-955-054A-121 (1-1102)

US-11-136-527-108
; Sequence 108, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 108
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-108

Alignment Scores:
Pred. No.:
Score: 4.02e-173   Length: 1643
                            1606.00   Matches: 319
Percent Similarity: 91.01%   Conservative: 5
                                             Mismatches: 10
Best Local Similarity: 89.61%   Indels: 22
Query Match: 86.02%   Gaps: 3
DB:

US-09-367-052-2 (1-359) x US-11-136-527-108 (1-1643)

Qy   4 IleSerValSerIleTyrThrSerAspAsnTyrSerGluValGlySerGlyAspTyr   23
         ||| ||:::::| |||||||||||||||||||||||||||||||
Db   38 ATTGCCATGGAAATATACACTTCGGATAACTACTACTCCGAGAAGTAGGTCTGGAGACTAT   97

Qy   24 AspSerAsnLysGluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeu   43
         |||||||||||||:|||:||
Db   98 GACTCCAACAAGGAACCCTGCTTCCGGGATGAAAACGAAAACTTCAACAGGATCTTCCTG   157

Qy   44 ProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeu   63
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 158 CCCACCATCTATTTTATCATCTTCTTGACTGGCATAGTGGGCAATGGGTTGGTAATCCTG   217

Qy   64 ValMetGlyTyrGlnLysLysLeuArgSerMetThrArgLysTyrArgLeuHisLeuSer   83
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 218 GTCATGGGTTACCAGAAGAAGCTGAGGAGCATGACAAGACAAGTACCGGCTGCACCTGTCC   277

Qy   84 ValAlaAspLeuLeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAsp   103
         ||||||||||||||||||||||||||||||| :
Db 278 GTGGCTGACCTCCTTTGTCATCACACTCCCCTTC-----AGTGACGCCATGGCTGAC   331

Qy 104 TrpTyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyr   123
         |||||||||||||||||||||||||||||||||||||||||||||
Db 332 TGGTACTTTGGGAAATTTTATGTAAGGCGTGCATATCATCTACACCGTCAACCTTTAC   391

Qy 124 SerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAla   143
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 392 AGCAGTGTTCTCATCCTGGCCTTCATCAGCCTGGACCGCTACCTTGCCATTGTCCACGCC   451

Qy 144 ThrAsnSerGlnArgProArgLysLeuLeuAlaGluLysValAlaValTyrValGlyValTrp   163
         ||||||||||||||||||||||||
Db 452 ACCAACAGCCAGAGGCCGCGGAAGCTGCTGGCTGAAAAGGCC-----------   493

Qy 164 IleProAlaLeuLeuLeuThrIleProAspPheIlePheAlaAspValSerGlnGlyAsp   183
         |||||||||||||
Db 494 ------------------------------GACATCATCTTCGCCGATGTC-------   514

Qy 184 IleSerGlnGlyAspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMet   203
         ||||||| ||||||||||||||||||
Db 515 --AGCCAGGGGGACGACGGGTACATCTGTGACAGGCTTTACCCGGACAGCCTGTGGATG   571

Qy 204 ValValPheGlnPheGlnHisIleMetValGlyLeuLeuLeuProValIleLeuLeu   223
         ||||||||||||||||||||||||||||||||
Db 572 GTGGTGTTCCAGTTCCAGCACATCATGGTGGGTCTCCTGCTGCCGGGCATCGTCATCCTG   631

Qy 224 SerCysTyrCysIleIleIleSerLysLeuSerHisGlnHisSerLysGlyHisGlnLeuSerGlyHisGlnLysGlyHisGlnLysArgLys   243
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 632 TCCTGTTACTGCATCATCATCTCCAAGCTGTCACACTCCAAGGGGCACCAGGAAGGCCAAG   691

Qy 244 AlaLeuLysThrThrValIleLeuValLeuLeuLeuAlaPhePheAlaCysTrpLeuProTyrTyr   263
         |||||||||||||||||||||||||||||||||||||||||||||||
Db 692 GCCCTCCAAGACTACGGTCATCCTTATCCTGGCTTCTTTGCCTGCTGGCTACCGTATTAC   751

Qy 264 ValGlyIleSerIleAspSerPheLeuLeuLeuGlyValIleLysGlyGlyCysAspPhe   283
         |||||||||||||||||||||||||||||||||||||||||||:::||
Db 752 GTGGGGATCAGCATCGATTCCTTCCTCATCCTTTGGAGGTCATCAAGGAGGATGTGAGTTC   811

Qy 284 GluSerIleValHisLysSerTrpIleSerIleThrGlnIleHisPheHisCysCys   303
         ||:|||||||||||||||||||||||||||||||||||||||||
Db 812 GAGAGCATCGTGCACAAGTCGGATCTCATCACGATCCATTTCCATTGCTGC   871

Qy 304 LeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerAlaGlnHisAla   323
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db 872 CTGAACCCCATCCTCTACGGCCTTCCTCGGGGCCAAATTCAAGASTCCGCAGCATGCA   931

Qy 324 LeuAsnSerMetSerArgGlySerSerLeuLysIleLeuSerLysGlyArgGlyGly   343
         |||||||||||||||||||||||||||||||||||||||||||||
Db 932 CTCAATTCCATGAGCAGAGGCTCAGCCTCCAGATCCTTTCCAAAGGGAAACGGGGTGGA   991

Qy 344 HisSerSerValSerThrGluSerSerGluSerSerPheHisSerSer   359
         |||||||||||||||||||||||||||||||||||||||||||
Db 992 CACTCTTCCGTCTCCACAGAGTCAGAATCCTCCAAGTTTTCACTCCAGC   1039

RESULT 8
US-11-136-527-6726
; Sequence 6726, Application US/11136527
; Publication No. US2005028757570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6726
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-6726

Alignment Scores:
Pred. No.:
Score: 1.46e-140   Length: 1400
                            1320.50   Matches: 257
Percent Similarity: 95.93%   Conservative: 2
                                             Mismatches: 6
Best Local Similarity: 95.19%   Indels: 5
Query Match: 70.73%   Gaps: 1
DB:

US-09-367-052-2 (1-359) x US-11-136-527-6726 (1-1400)

Qy   90 ValIleThrLeuProPheTrpAlaValAspAlaMetAlaMetAlaAspTrpTyrPheGlyLysPhe   109
         ||||||||||||||||||||||||| ||||||||||||||||
Db   2 GTCATCACACTCCCCTTCTCGGGCAGTGGACGTGGACTGGTACTTTGGGAAATTT   61

Qy 110 LeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIleLeu   129
         ||||||||||||||||||||||||||||||||||||||||||||
Db   62 TTATTGTAAGGCTGTGCATATCATCTACACCGTCAACCTTTACAGCAGTGTTCTCATCCTG   121

Qy 130 AlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGlnArgPro   149
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 122 GCCTTCATCAGCCTGGACCGCTACCTTGCCATTGTCCACGCCACCAACAGCCAGAGGCCG   181

Qy 150 ArgLysLeuLeuAlaGluLysValAlaLysValAlaValTyrValGlyValValTrpIleProAlaLeuLeuLeu   169
         ||||||||||||||||||||||||
Db 150 GTGGTGTTCCAGTTCCAGCACATCATGGTGGGTCTCCTGCTGCCGGGCATCGTCATCCTG   631

```
Db   182  AGGAAGCTCTGGCTGGTGAAAAGGCCGTCATGTGGTGGTGGATCCCCCTG  241
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    73  SerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeuLeuPheValIleThr  92

Qy   170  ThrIleProAspPheIleProAlaAspPheAlaAspValSerGlnGlyAspIleGlyAspAsp  189
          |||||||||||||||||||||||||||||||||---------
Db    62  CTCCCCTTC------AGTGACGCCATGGCTGACTCGTACTTTGGGAAATTTTATGTAAG  115
Qy    93  LeuProPheTrpAlaValAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys  112

Qy   242  ACTATCCCTGACATCATCTTCGCCGATGTC------------AGCCAGGGGGACGGC  286
          ||||||||||||||||||||||||||||||
Db   116  GCTGTGCATATCATCTCACCGTCAACCTTTACAGCAGTGTTCTCATCCTGGCCTTCATC  175
Qy   113  AlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeuIleLeuAlaPheIle  132

Qy   190  ArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPheGln  209
          |||||||||||||||||||||
Db   176  AGCCTGGACCGGCTACCTTGCCATTGTCCACGCCACCAACAGCCAGAGCGCGAGGAAGCTG  235
Qy   133  SerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGlnSerGlnArgProArgLysLeu  152

Qy   287  AGGTACATCTGTGACCGGCTTTACCCCGACAGCCTGTGGATGGTGGTGTTCCAGTTCCAG  346
          |||||||||||||||||||||||||||||||
Db   236  CTGGCTGAAAAGGCC------  250
Qy   153  LeuAlaGluLysAlaValAlaTyrValGlyValTrpIleValTrpIleProAlaLeuLeuLeuThrIlePro  172

Qy   210  HisIleMetValGlyLeuLeuLeuProGlyIleLeuValIleLeuSerCysTyrCysIleIle  229
          |||||||||||||||||||||||||||||
Db   251  GACATCATCTTCGCCGATGTC------------AGCCAGGGGGACGGCAGGGTACATC  295
Qy   173  AspPheIleAlaAspValSerGlnGlyAspIleSerGlnGlyAspIleSerGlnGlyAspArgTyrIle  192

Qy   347  CACATCATGTGGGTCTCATCCTGCCGGGCATCGTCATCCTGTGTGTCATCGTCATCATCCTCCAAG  406
          |||||||||||||||||||||||||||||||||||||
Db   296  TGTGACCGGCTTTACCCCGACAGCCTGTGGATGGTGGTGTTCCAGTTCCAGCACATCATG  355
Qy   193  CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnPheGlnHisHisIleMet  212

Qy   230  IleSerLysLeuSerHisSerLysGlyHisSerGlnLysSerArgLysAlaLeuLysThrThrVal  249
          ||||||||||||||||||||||||||||||||||
Db   356  GTGGGTCTCATCCTGCCGGGCATCGTCATCCTGTGTGTCATCGTCATCTCCAAG  415
Qy   213  ValGlyLeuLeuLeuProGlyIleLeuValIleLeuSerCysTyrCysIleIleIleSerLys  232

Qy   407  ATCTCCAAGCTGTCACACTCCAAAGGGCCACCAGAGCGCCAAGGCCCTCAAGACTACGGTC  466
          |||||||||||||||||||||||||||||||||||||||||
Db   416  CTGTCACACTCCAAAGGGCCCACCAGAGAGGCGCAAGGCCCTCAAGACTACGGTCATCGTCATC  475
Qy   233  LeuSerHisSerLysGlyHisSerGlnLysSerArgLysAlaLeuLysThrThrValIleLeuIle  252

Qy   250  IleLeuIleLeuAlaPheAlaCysTyrTrpLeuProTyrTyrValGlyIleSerIleAsp  269
          ||||||||||||||||||||||||||||
Db   476  CTGGCTTTCTTTGCCTGCTGCTGGCTACCGTATTACGTGGGATCAGCATCGATTCCTTCATC  535
Qy   253  LeuAlaPheAlaCysTyrTrpLeuProTyrTyrValGlyIleSerIleAspSerPhePhe  272

Qy   467  ATCCTTATCCTGGCTTTCTTTGCCTGCTGCTGGCTACCGTATTACGTGGGATCAGCATCGAT  526
          |||||||||||||||||||||||||||||::::||||||||
Db   536  CTTTTGGAGGTCATCAAGCAAGGAATGTGAGTTCGAGAGCGTCGTGCACAAGTGGGATCTCC  595
Qy   273  LeuLeuGlyValIleLysGlnGlyGlyCysAspPheGluSerIleValHisLysTrpIleSer  292

Qy   270  SerPheLeuLeuLeuGlyValIleLeuLysGlnGlyGlyCysGlnGlyAspPheGluSerIleValHisLys  289
          |||||||||||||||||||||||::::||||||
Db   596  ATCACGGAGGCCCTGCCTTCTTCCCACTGKTGCCTGCCCATCCTCTACGCCTTCCTC  655
Qy   293  IleThrGluAlaLeuAlaPheHisCysCysLeuAsnProIleLeuTyrAlaPheLeu  312

Qy   527  TCCTTCATCCTTTTGGAGGTCATCAAGCAAGGAATGTGAGTTCGAGAGCGTCGTGCACRAG  586
          |||||||||||||||||||||||::::||||||
Db   656  GGGGCCCAAATTCAAGAGASTCCGCGACAATGCAGTCACTCAATTCCATGAGCAGAGGCTCCAGC  715
Qy   313  GlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSerArgGlySerSer  332

Qy   290  TrpProIleSerIleThrGluAlaLeuAlaLeuAlaPheHisCysCysLeuAsnProIleLeuTyr  309
          ||||||||||||||||||||||||||||||||
Db   716  CTCAAGATCCTTTCCAAAGGGAAACGGGGGTGGACACTCTTCCGTCCCAGAGTCAGAA  775
Qy   333  LeuLysIleLeuSerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu  352

Qy   587  TGGATCTCCATCACGGAGGCCCTGCCTTCTTCCCACTGTGCCTGAACCCCATCCTCTAC  646
          ||||||||||||||||||||||||||||||||||||||
Db   776  TCCTCAAGTTTTCACTCCAGC  796
Qy   353  SerSerSerPheHisSerSer  359

Qy   310  AlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSerArg  329
          |||||||||||||||||||||||||||||||||
Db   647  GCCCTTCCTCGGGGCCCAAATTCAAGAGASTCCGCGACAATGCAGTCACTCAATTCCATGAGCAGA  706

Qy   330  GlySerSerLeuLysIleLeuSerLysGlyLysArgGlyGlyHisSerSerValSerThr  349
          |||||||||||||||||||||||||||||||||||
Db   707  GGCTCCAGCCTCAAGATCCTTTCCAAAGGGAAACGGGGTGGACACTCTTCCGTCCCACA  766

Qy   350  GlySerGluSerSerSerPheHisSerSer  359
          ||||||||||||||||||||||
Db   767  GAGTCAGAGATCCTCAAGTTTTCACTCCAGC  796
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RESULT 9
US-11-136-527-4204

; Sequence 4204, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 36830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4204
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-4204

Alignment Scores:
Pred. No.:
Score: 1.48e-134   Length: 1400
                       1268.00   Matches: 255
Percent Similarity: 89.55%   Conservative: 2
Best Local Similarity: 88.85%   Mismatches: 8
Query Match: 67.92%   Indels: 22
DB: Gaps: 3

US-09-367-052-2 (1-359) x US-11-136-527-4204 (1-1400)

RESULT 10
US-11-136-527-153

; Sequence 153, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294

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; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 153
;  LENGTH: 1680
;  TYPE: DNA
;  ORGANISM: Rattus norvegicus
US-11-136-527-153

Alignment Scores:
Pred. No.:              2.5e-57      Length:         1680
Score:                  594.00       Matches:        123
Percent Similarity:     54.60%       Conservative:   67
Best Local Similarity:  35.34%       Mismatches:     138
Query Match:            31.82%       Indels:         20
DB:                                  Gaps:           4

US-09-367-052-2 (1-359) x US-11-136-527-153 (1-1680)

Qy   17  GluValGlySerGlyAspTyrAsp------------------SerAsnLysGlu   28
             :::                                       ::::::
Db  209  GAAAACAGACATCTCCCTACGGATTATGGGAAAAMRAAARMRAMWMWMWCTGACTCCCG  268

Qy   29  ProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPhe   48
          ||||| ||                ::   ::::::||||  ||||| ||||||||||||
Db  269  CCCTGCCCACAGACTTCAGCTGAACTTGACAGAACCTTCCTGCCAGTCCTCTACAGC  328

Qy   49  IleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMetGlyTyrGln   68
          :::||||||  || ||||||||||| ||    |||   :::  ||
Db  329  CTCCRCTTTTGTCGGGCTGCTAGGCAATGGGGCAGTGCTGCTGTGCTACTGAGCCAG  388

Qy   69  LysLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeuLeu   88
          ::: ||||||||||||||||||:::||||||::: ::||||||||||
Db  389  CGGCACTGCCCTGAGCACAGCAGACACCTTCCTGCTTCCACCTGGCTGTGCCGATGTACTG  448

Qy   89  PheVallleThrLeuProPheThrTrpAlaValAlaAspAlaMetAlaAspTrpTyrPheGlyLys  108
          :::
Db  449  CTGGTACTAACCCTCCCACTGTGGGCAGTAGATGCTGCTGCCCAGTGGGTTTCGGCTCT  508

Qy  109  PheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerValLeuIle  128
          |||||:::            ::::||  || :::|||
Db  509  GGTCTCTGCAAAGTGGCCAGATCAACATCAACTTCTACGCAGGGGCCTTCCTG  568

Qy  129  LeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGlnArg  148
          ||||  | |  ||||||||||||||| ||||||    :::   :::
Db  569  CTGGCCTGATAAGCTTTGACCGCTACCTGGCTACCAGTAGTGCATGCGCACCCAGATCTACCGC  628

Qy  149  ProArgLysLeuLeuAlaGluLysGlyLysAlaValTyrValGlyValTrpIleProAlaLeuLeu  168
          :::
Db  629  AGGGACCCCTGGGTACGTGTAGCCCTCACCTGCCATTGTGTGTGGGGTCTCTGTGTGCTC  688

Qy  169  LeuThrIleProAspPheIlePheAlaAspAspIleSerGlnIleGlyAsp  188
          ::::||| |||  |||||||||||
Db  689  TTTGCCCTCCAGATTTCATCTTCCTGTCCAGCCAGCCAT-------GATCAGCAGCTC  739

Qy  189  AspArgTyrIleCysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnInPhe  208
          :::
Db  740  AATGCCACCCATTGCCAGTACAACTTCCCA---CAGGTGGGTCGGACTGCTCTGCGTGTA  796

Qy  209  GlnHisHisMetValGlyLeuLeuIleLeuProGlyIleValLeuLeuSerCysTyrCysIleLys  228
          :::
Db  797  CTGCAGCTAGTGGCTGGTTTCCTGATGCCCCTTCTAGTCATGGCCTACTGCTATGCCCAT  856

Qy  229  IleIleSerLysLeuSerHisSerLysArgGlnLysLysAlaLeuLysLysThrThr  248
          |||||:::     ::::||  ||
Db  857  ATCCTGGTGTGCTGTGCGTTTGCCTTGCTCTGCTGGAGGCGCTATGAGGCTAGTG  916

Qy  249  ValIleLeuIleLeuAlaPheAlaCysTrpLeuProTyrTyrValGlyIleSerIle  268
          |||||||||||||||||| |||||||||||:::||||||||||
Db  917  GTGTGGTGGTGGTGCCCTTTGCCGTCTGCTGGACCCCCATCACCTGGGTTGGTTTAGTG  976

Qy  269  AspSerPheLeuLeuGlyValIleLeuLysGlnGlyCysAspPheGluSerIleValHis  288
          |||||| ||||||||||
Db  977  AGCTTTGACCGCTACCTGGCCATGATGTCATGCGACCCCAGATCTACCGCAGGGACCCCTGG  1036
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Qy  289  LysTrpIleSerIleThrGluAlaLeuAlaPheHisCysCysLeuAsnProIleLeu  308
          |||||:::||||| |::|||||||  ||||||||||||:::||:::||
Db 1037  GTAGCCAAGTCAGTCACCTCAGGCATGGCACTGCTGCCTCAATCACTCACTGCTC  1096

Qy  309  TyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSer  328
          ||||||||||||:::||| ||||||||
Db 1097  TATGCCTTTGTGGGAGTGAAGTTCAAAGAACAAATGTGATGTGTCATGCGCTGGGC  1156

Qy  329  ArgGlySerSerLeuLysIleLeuSerLysGlyLysHisSerSerValSer  348
          ||                              ----------
Db 1157  CGCTCTGAC---------------------------CAGAGAGGMCCCAGCGCGCAGCCTCA  1192

Qy  349  ThrGluSerGluSerSerPhe  356
          :::   |||:::
Db 1193  TCTTCACGGAGAAATCATCCTGG  1216
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RESULT 11
US-11-136-527-4249
; Sequence 4249, Application US/11136527
; Publication No. US2005028757OAl
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT: Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE: 2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4249
;  LENGTH: 1400
;  TYPE: DNA
;  ORGANISM: Rattus norvegicus
US-11-136-527-4249

Alignment Scores:
Pred. No.:              2.2e-55      Length:         1400
Score:                  576.00       Matches:        117
Percent Similarity:     55.86%       Conservative:   64
Best Local Similarity:  36.11%       Mismatches:     131
Query Match:            30.85%       Indels:         12
DB:                                  Gaps:           3

US-09-367-052-2 (1-359) x US-11-136-527-4249 (1-1400)

Qy   33  AspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyrPheIleIlePheLeu   52
           | ||                       ||   :::   :::||||
Db    1  GACTTTCAGCTGAACTTGACAGAACCTTCTGCCAGTCCTCAGCCTCCTCTTTTTG   60

Qy   53  ThrGlyIleValGlyAsnGlyLeuValIleLeuValMetGlyTyrGlnLysLysLeuArg   72
          |||:::||||||||||||||||||||| |||   :::||||||||||
Db   61  CTGGGGCTGCTAGGCAATGGGCAGTGGCCAGTGCTGCTGAGCCAGGCACTGCCCTG  120

Qy   73  SerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeuLeuPheValIleThr   92
          ::: ||||||||||||||||||:::||||||::: ::||||||
Db  121  AGCAGCCACAGACACCTTCCTGCTCCACCTGGCTGTGGCCGATGTACTGTTCGTACTAACC  180

Qy   93  LeuProPheTrpAlaValAlaAspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLys  112
          ::::||| |||:::
Db  181  CTCCCACTGTGGGCAGTAGATGCTGCCCAGTGGGTTTCGGCTGTCTCTGCAAA  240

Qy  113  AlaValHisIleIleTyrThrValAsnLeuTyrSerValLeuIleLeuAlaPheIle  132
          :::::::||  || :::|||||||| |
Db  241  GTGGCCCATCATCAACTTCTACAGCGAGGGCCTTCCTGCTGGCCTTTGCCTGTGTATA  300

Qy  133  SerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGlnArgProArgLysLeu  152
          ||||||||||||| ||||||    ::: :::
Db  301  AGCTTTGACCGCTACCTGGCATTAGTGCATGCGACCCCAGATTCTACCGCAGGGACCCCTGG  360
```

US-09-367-052-2 (1-359) x US-11-136-527-2373 (1-1324)

```
Qy      12 AspAsnTyrSer--GluGluValGlySerGlyAspTyrAsp----------------- 24
           |||||||:||  ::  ||||:|
Db     150 GATAATTCAGCCTTGAAGACTTCTCAGTGGAGATATTGACAGTTACAATTACAGTTCT 209

Qy      25 ----------------SerAsnLysGluProCysPheArgAspGluAsnValHisPhe 38
                           ||||||||||
Db     210 GACCCGCCCTTACTCTGTCAGATGCTGCCCCATGC---CCCTCAGCGAACCTAGATATC 266

Qy      39 AsnArgIlePheLeuProThrIleTyrPheIleIlePheLeuThrGlyIleValGlyAsn 58
           ||||||           :::           ::::::
Db     267 AACAGGTATGCTGGTTGTCATATACGTTCTGGTGACTTTGCTGAGTCTCGTGGGGAAC 326

Qy      59 GlyLeuValIleLeuValMetGlyTyrTyrGlnLysLysLeuArgSerMetThrAspLysTyr 78
           ||||:|||||:|||:|||
Db     327 TCCCTGGTGATGCTGTCATCTTGTACAATCGAAGCACCTGCTCTGTTACCGAGTCTAC 386

Qy      79 ArgLeuHisLeuSerValAlaAspLeuLeuPheValIleThrLeuProPheTrpAlaVal 98
           ||||||||||||||:::||||||
Db     387 CTGCTGAACCTGGCCATTGTGATCTGTTCTTTGCCCTGACCTTGCCTGCTGGGGTGCA 446

Qy      99 AspAlaMetAlaAspTrpTyrPheGlyLysPheLeuCysLysAlaValHisIleIleTyr 118
           :::                  ||||||          :::
Db     447 TCTAAAGTAAATGGATGATTTTTGGCTCATTCCTGTGCAAGGTATTCTCGTTCCTGCAG 506

Qy     119 ThrValAsnLeuTyrSerSerValLeuIleLeuAlaPheIleSerLeuAspArgTyrLeu 138
           :::
Db     507 GAGATTACCTTCTACAGCAGTGTTCTGTTCTGTGTCTAGCCTGCATGAGACCTACCTG 566

Qy     139 AlaIleLeuValHisAlaThrAsnSerGlnArgProArgLysLeuLeuAlaGluLysAlaVal 158
           :::                     |||   ::::::
Db     567 GCCATCGTCCAGCCACAAGTACACTGATCAGAAGAGAGACACTTGGTC--AAGTTGTG 623

Qy     159 TyrValGlyValTrpIleProAlaLeuLeuLeuThrIleProAspPheIlePheAlaAsp 178
           |||          ||||||
Db     624 TGCATCACCATGTGGTTTCCTCCACTAGTTCTGTCCTGGCCCATCTTCATTCTT------ 677

Qy     179 ValSerGlnGlyAspIleSerGlnGlyAspAspAlaArgTyrIleCysAspArgLeuTyrPro 198
           :::
Db     678 ------CGGACTACTGTTAAGGCAACCCTTCACCGTAGTCGC--------TATGAG 722

Qy     199 Asp-----------------SerLeuTrpMetValValPheGlnInPheGlnHisIleMetVal 213
           :::
Db     723 AATATAGGTAATATACATCAAGTGGAGGTGGTACTGGCATCCTGCCTCAGACCTAT 782

Qy     214 GlyLeuIleLeuProGlyIleValGlyIleValLeuLeuSerCysTyrCysIleIleSerLeuSerLysLeu 233
           ||| :::||        ::::::
Db     783 GGCTTCCTCCTGCCTGCTCATCATGGTGTTCTGCTATGGGTTCACACTGCGCACGCTC 842

Qy     234 SerHisSerLysGlyHisGlnLeuArgLysAlaLeuLysAlaLeuLeuThrValIleLeuLeuLeu 253
           :::                  ::::::
Db     843 TTTAAGGCCCACATGGGGCAGAAGCACCGGGCCATGCGGCCATCTTTGCTGTGGTCCTC 902

Qy     254 AlaPheAlaCysPheTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIleLeu 273
           ||| :::                  ::::::
Db     903 GTCTTCCTGCTCTGCTGGGCTTCCCATAACATTGCTCCTGTTCACAGACACCCTCATGAGA 962

Qy     274 LeuGlyValIleLeuValLeuGlyCysGluSerIleValHisLysTrpIleSerIle 293
           ||| |||       ::::::
Db     963 ACCAAGCTGATCAAGGAGACCTGTGAACGCCAGAACGAGATTAACAAAGCTTTGGAAGCT 1022

Qy     294 ThrGluValAlaLeuAlaPhePheHisCysCysLeuAsnProIleLeuTyrAlaPheLeuGly 313
           ||| :::||               ::::::
Db    1023 ACTGAGATTCTTGGCTTCCTCCACAGCTGTTTAACCCCATCATCTATGCCTTTATTGGC 1082

Qy     314 AlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSerArgGlySerSerLeu 333
           ||| :::||
Db    1083 CAGAAATTTCGC--------------CATGGACTT---------------CTC 1106

Qy     334 LysIleLeuSerLys----------------GlyLysArgGlyGlyHis 344
           :::||
Db    1107 AAGATCATGGCTAATTATGGCCTTGTCAGCAAGGAGTTCTTAGCCAAGGAGGCCAGGCCT 1166
```

```
Qy     153 LeuAlaGluLysAlaValAlaTyrValGlyValTrpIleProAlaLeuLeuLeuThrIlePro 172
           :::                  ::||||||
Db     361 GTAGTGTAGCCCTCACCTGTTGTGTGGGGTCTCTGCTCCTTGCCCTCCCA 420

Qy     173 AspPheIleAlaAspValSerGlnGlyAspIleSerGlnGlyAspAspAlaArgTyrIle 192
           ||||||||||
Db     421 GATTTCATCTTCCTGTCAGCCAGCCAT------GATCAGGCGCCTCAATGCCACCCAT 471

Qy     193 CysAspArgLeuTyrProAspSerLeuTrpMetValValPheGlnHisIleIleMet 212
           :::
Db     472 TGCCAGTACAACTTCCCA---CAGGTGGGTCGGACTACTGTGCGTACTGCAGCTAGTG 528

Qy     213 ValGlyLeuIleLeuProGlyIleValIleLeuValLeuSerCysTyrCysIleIleLeuSerLys 232
           ||| :::||
Db     529 GTGTGTTCCTGATGCCCCTTCTAGTCATGGCCTACTGCTATGCCCATATCCTGGCTGTG 588

Qy     233 LeuSerHisSerLysGlyHisGlnLeuArgLysArgLysAlaLeuLysThrThrValIleLeuLeuIle 252
           :::                  ::::::
Db     589 CTGCTGGTCTCCAGAGGCCAGAGCGCTTTCGAGCTATGAGGTGGTGGTGGTGGGTG 648

Qy     253 LeuAlaPheAlaCysPheTrpLeuProTyrTyrValGlyIleSerIleAspSerPheIle 272
           :::||||||          :::
Db     649 GTGGCCCTTTGCCGTCTGGACCCCCTATCACCTGGTGTGTTAGTGGATATCCTTATG 708

Qy     273 LeuLeuGlyValIleLeuValLeuGlyGlnGlySerIleValHisLysTrpIleSer 292
           :::||
Db     709 GACGTGGAGTTTTGGCCCCGCAACTGTGTCGAGAAAGCCATGTGGACGTAGCCAAGTCA 768

Qy     293 IleThrGluValAlaLeuAlaPhePheHisCysCysLeuAsnProIleLeuTyrTyrAlaPheLeu 312
           ::: :::                  ::::::
Db     769 GTCACCTCAGGCATGGGCTACATGGGCCACATCCACTGCTCTATGCCTTTGTG 828

Qy     313 GlyAlaLysPheLysSerSerAlaGlnHisAlaLeuAsnSerMetSerArgGlySerSer 332
           :::||              |||
Db     829 GGAGTGAAGTTCAAGAACAAATGGGATGTTGCTCATGCGCCTGGGCGTCTGAC--- 885

Qy     333 LeuLysIleLeuSerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGlu 352
           :::||||||
Db     886 ----------------------------------CAGAGAGMCCGCAGCCAGCCTTCATCTTCACGGAGA 924

Qy     353 SerSerSerPhe 356
           :::|||
Db     925 GAATCATCCTGG 936
```

RESULT 12

US-11-136-527-2373

```
; Sequence 2373, Application US/11136527
; Publication No. US2005028757OA1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT: Mounts, William M
;  TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
;  FILE REFERENCE: 031896-041000 (AM101086)
;  CURRENT APPLICATION NUMBER: US/11/136,527
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US 60/574,294
;  PRIOR FILING DATE: 2005-05-26
;  NUMBER OF SEQ ID NOS: 362830
;  SOFTWARE: PatentIn version 3.2
;  SEQ ID NO 2373
;  LENGTH: 1324
;  TYPE: DNA
;  ORGANISM: Rattus norvegicus
US-11-136-527-2373
```

Alignment Scores:
```
Pred. No.:                         Length:        1324
Score:            8.09e-54         Matches:       130
Percent Similarity:  53.10%        Conservative:   67
Best Local Similarity:  35.04%     Mismatches:    126
Query Match:      30.10%           Indels:         48
                                   Gaps:           10
DB:                                                7
```

```
Qy    345  SerSerValSerThrGluSerSerSer 355
           ||| ::|||||||||||||||||||
Db   1167  TCTTTTGTTGGCTCTTTTCAGCGAACACTCC 1199

RESULT 13
US-10-775-169-254
; Sequence 254, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT: Burczynski, Michael
;  APPLICANT: Twine, Natalie
;  APPLICANT: Dorner, Andrew
;  APPLICANT: Trepicchio, William
;  TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
;  FILE REFERENCE: AM.01080 (031896-013000)
;  CURRENT APPLICATION NUMBER: US/10/775,169
;  CURRENT FILING DATE: 2004-02-11
;  NUMBER OF SEQ ID NOS: 5278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 254
;  LENGTH: 3100
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-775-169-254

Alignment Scores:
Pred. No.:           9.28e-51      Length:            3100
Score:               540.00        Matches:            121
Percent Similarity:  51.09%        Conservative:       147
Best Local Similarity: 33.06%      Mismatches:          32
Query Match:         28.92%        Indels:               7
DB:                                Gaps:                 6

US-09-367-052-2 (1-359) x US-10-775-169-254 (1-3100)

Qy     9  TyrThrSerAspAsnTyrSerGluGluValGlySerGly--AspTyrAspSerAsnLys 27
          ::: |||:||||||||:::|||||||||||   ||:||||||||::
Db    82  TTCACCATGGATCAGTTCCCTGAATCAGTGACAGAAAACTTGAGTACGATGATTTGGCT 141

Qy    28  GluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyr 47
          |||||||            ::|||||||||||||||
Db   142  GAGGCCTGTTATATTGGGGACATCGTGGTCTTTGGGACTGTGTTCCTGTCCATATTCTAC 201

Qy    48  PheIleIlePheLeuThrGlyIleValGlyAsnGlyLeuValIleLeuValMetGlyTyr 67
          |||:||||||||          :::|||||||
Db   202  TCCGTCATCTTTGGCCATTGGCCTGGTGGGAAATTTGTTGGTAGTGTTTGCCCTCACCAAC 261

Qy    68  GlnLysLeuArgSerMetThrAspLysTyrArgLeuHisLeuSerValAlaAspLeu 87
          :::|||||||
Db   262  AGCAAGAGAGCCCAAGAGTGTCACCGACATTTACCTCCTGGACCTTGTCTGATCTG 321

Qy    88  LeuPheValIleThrLeuProPheTrpAlaValAspAlaMetAlaAspTrpTyrPheGly 107
          |||||||
Db   322  CTGTTTGTAGCCACTTTGCCCTTCTGGACTCACTATTTGATAAATGAAAAGGGCCTCCAC 381

Qy   108  LysPheLeuCysLysAlaValHisIleIleTyrThrValAsnLeuTyrSerSerValLeu 127
          ::|||||||                           ||:|||
Db   382  AATGCCATGTCAAATTCACTACCACCGGTCCTTCTCATCGGGCTTTTTCGGAAGCATATTC 441

Qy   128  IleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSerGln 147
          |||||||
Db   442  TTCATCACCGTCATCAGCATTGATAGGTACCTGGCCATCGTCCTGGCCGCCAACTCCATG 501

Qy   148  ArgProArgLysLeuLeuAlaGluLysValValAlaTyrValGlyValTrpIleProAlaLeu 167
          ::: :||||||
Db   502  AACAACCGGACCTGCAGCATGGCGTCACCATAGCGTCTCTAGGCGGCAGCAGCCATT 561

Qy   168  LeuLeuThrIleProAspPheIlePheAlaAspValSerGlnIleSerGlnGly 187
          |||:|||:|||
Db   562  TTGGTGGCAGCACCCAGTTCATGTTCACAAAGCAAAGCAGAAAATGAA------------ 609
```

```
Qy   188  AspAspArgTyrIleCysAspArgLeuTyrProAsp------SerLeuTrpMetVal 204
          |||:                    :: ||||||
Db   610  ------TGCCTTGGTGACTACCCGAGGTCCTCCAGGAAATCTGGCCCGTG 654

Qy   205  ValPheGlnPheGlnHisIleMetValGlyLeuLeuLeuProGlyIleValIleLeuSer 224
          :|||                                  :::|||||||
Db   655  CTCCCGCAATGTGGAACAAATTTCTTGGTGCTTCCTACTCCCCTGCTCATTATGAGTTAT 714

Qy   225  CysTyrCysIleIleIleIleSerLysLeuSerHisSerLysGlyHisGlnLysArgLysAla 244
          |||:||||||||                              :||||||
Db   715  TGCTACTTCAGAATCATCCAGACGCTGTTTCCTGCAGAACCACAAGAAAGCCAAAGCC 774

Qy   245  LeuLysThrThrValIleLeuIleLeuAlaAlaPheCysTrpLeuProTyrTyrVal 264
          :::|||                    ::::|||||||||||
Db   775  ATTAAAACTGATCCTTCGTGGTCATCGTGTTTTCCTCTTCTGGACACCCTACCAACGTT 834

Qy   265  GlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnCysAspAspPheGlu 284
          :::|||                      :||||||
Db   835  ATGATTTTCCTGGAGACGCTTAAGCTCTATGACTTCTTT---CCCAGTTGTGACATGAGG 891

Qy   285  SerIleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHisCysCysLeu 304
          |||:||                       ::|||||||
Db   892  AAGGATCTGAGGCTGCCCCTCAGTGACTGAGACGGTGCATTTAGCATTGTTGCCTG 951

Qy   305  AsnProLeuLeuTyrAlaPheLeuGlyLeuLysPheArgArgArgLysSerArgAlaGlnHisHisAlaLeu 324
          |||||:::|||::                :||::|||
Db   952  AATCCTCTCATCTATGCATTGCTGGGGAGAAGTTCAGAAGATACCTTTACCACTGTAT 1011

Qy   325  AsnSerMetSerArgGlySerArgLeuLysIleLeu 336
          :::||||::
Db  1012  ------GGGAAATGCTGGCTGTCCCTGTGTGGGCCTCAGTCCACGTTGAT 1056

Qy   337  ------SerLysGlyLysArgGlyGlyHisSerSerValSerThrGluSerGluSer 353
          |||:||                 :|||||||
Db  1057  TTCTCCTCATCTGAATCACAAAGAGCAGCAGGCATGGAAGTGTTCTG-----AGCACAAT 1110

Qy   354  SerSerPheHisSerSer 359
          :::|||||:::|||
Db  1111  TTTACTTACCACGAGT 1128

RESULT 14
US-11-127-877-25
; Sequence 25, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
;  APPLICANT: Merchiers, Pascal G.
;  APPLICANT: Hoffmann, Marcel
;  APPLICANT: Spittaels, Koenraad F. F.
;  APPLICANT: Laenen, Wendy
;  TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;  TITLE OF INVENTION: Amyloid-Beta Protein Production
;  FILE REFERENCE: P27,800-B USA
;  CURRENT APPLICATION NUMBER: US/11/127,877
;  CURRENT FILING DATE: 2005-05-12
;  PRIOR APPLICATION NUMBER: 60/570,352
;  PRIOR FILING DATE: 2004-05-12
;  PRIOR APPLICATION NUMBER: 60/603,948
;  PRIOR FILING DATE: 2004-08-24
;  NUMBER OF SEQ ID NOS: 590
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
;  LENGTH: 3177
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-11-127-877-25

Alignment Scores:
Pred. No.:           3.59e-50      Length:            3177
Score:               535.00        Matches:            124
Percent Similarity:  53.55%        Conservative:        72
Best Local Similarity: 33.88%      Mismatches:         136
Query Match:         28.66%        Indels:              34
DB:                                Gaps:                 9
```

US-09-367-052-2 (1-359) x US-11-127-877-25 (1-3177)

```
Qy    10  ThrSerAspAsnTyrSerGluGlyValGlySerGlyAspTyr-----AspSerAsnLys  27
              :::|||||:::|||||||  ::  :|||||||  :
Db   306  TCCAGTGAAGATTATTTTGTCAGTCAATACTTCATATTACTCAGTTGATTCTGAGATG  365

Qy    28  GluProCysPheArgAspGluAsnValHisPheAsnArgIlePheLeuProThrIleTyr  47
              |||||||||||:::|||  |||  |||||||  ::  |||
Db   366  TTACTGTGCTCCTTGCAGGAGGTCAGGCAGTTCTCCAGGCTATTTGTACCGATTGCCTAC  425

Qy    48  PheIleIlePheLeuThrGlyIleValGlyLeuValIleLeuValMetGlyTyr  67
              :::|||  :::  |||||||||  :::
Db   426  TCCTTGATCTGTGTCTTTGGCCTCTGGGGAATATTCTGGTGGTGATCACCTTTGCTTTT  485

Qy    68  GlnLysGlyLeuLysArgSerMetThrAspTyrArgLeuHisLeuSerValAlaAspLeu  87
              |||:::|||||  ::  |||||||  ::  |||
Db   486  TATAGAAGGCCAGTCTATGACGACGTCTATCTTCTTGAACATGGCCATTGCAGACATC  545

Qy    88  LeuPheValIleThrLeuProPheThrProAlaValAsp---AlaMetAlaAspTrpTyrPhe  106
              |||  |||||||  ::  :::  |||
Db   546  CTCTTTGTTCTTACTCTCCCATTCTCGGCAGTGAGTCATGCCACCGGTGCGTGGGTTTC  605

Qy   107  GlyLysPheLeuCysLysPheAlaValHisIleLeuIleTyrThrValAsnLeuTyrSerVal  126
              |||||||:::  :::
Db   606  AGCAATGCCACGTGCAAGTTGCTAAAAGGCCATCTATGCCATCAACTTTAACTGCGGGATG  665

Qy   127  LeuIleLeuAlaPheIleSerLeuAspArgTyrLeuAlaIleValHisAlaThrAsnSer  146
              |||||||  :::|||
Db   666  CTGCTCCTTGCACTTGCCATTGACCGGTACACTGGCGACTAAGTCA  725

Qy   147  -----GlnArgProArgLysLeuLeuAlaAlaGluLysArgAlaValTyrValGlyValTrpIle  164
              |||  :::  :::  |||
Db   726  TTCCGGCTCCGATCCAGAACACTACCGCGCCAGCAAATCATCTGCCTTGTTGTGTGGGGG  785

Qy   165  ProAlaLeuLeuThrIleProPheAlaIleProPheAlaAspValSerGlnValGlyAspIle  184
              :::|||:::|||  ::  |||
Db   786  CGTGTCAGTCGTCATCATCCCAGCTCCAACTTTGTCTTC------AACCAAAAATACAAC  836

Qy   185  SerGlnGlySerIleValHisLysAspAspArgTyrIleCysAspArgLeuTyr  200
              :::|||  ||||||  :::  |||
Db   837  ACCCAAGGCAGGCGAT------GTCTGTGAACCCAAGTACCGGAGCCCCATC  890

Qy   201  LeuTrpMetValValPheGlnGlnPheAlaValMetValGlyLeuLeuLeuProGlyIle  220
              |||||||  :::  :::|||
Db   891  AGGTGGAAGCTGCTGATGTTGGGGCTGGGCTACTCTTTGGTTTCTTTATCCCCTTTGATG  950

Qy   221  ValIleLeuSerCysTyrCysIleIleIleSerLysLeuSerHisSerLysSerGlyHisGln  240
              :::|||  :::  |||
Db   951  TTCATGATATTTTGTTACGTTCATTGTCAAGCTCCAGAATTCTAAA  1010

Qy   241  LysArgLysLeuAlaLeuLysThrThrValIleLeuIleLeuAlaPheGlyAlaCysTrpLeu  260
              |||||||  :::  :::|||
Db  1011  AGGCACAAAGCCATCCGTAATCATCGTCGTGTTTCTGCTTGTCAGATT  1070

Qy   261  ProTyrTyrValGlyIleSerIleAspGluSerLeuLeuLeuGlyValIleLysGlnGly  280
              |||||||  :::  :::
Db  1071  CCTCATAACATGGTCCTGCTTGTGACGGCT---GCAAATTGGGTAAAATGAACCGATCC  1127

Qy   281  CysAspPheGluSerIleIleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhe  300
              |||||||  :::  :::|||
Db  1128  TGCCAGAGCGAAAGCTAATTGGCTATACGAAAAACTGTCACAGAAGTCCTGGCTTTCCTG  1187

Qy   301  HisCysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAla  320
              |||  ::  |||||||
Db  1188  CACTGCTGCCTGAACCCTATCCTGTATGCCTTCTTATTGGGCAGAAGTTC----  1235

Qy   321  GlnHisAlaLeuAsnSerMetSerArgGlySerLeuLysIleLeuSer---------  337
              :::  :::  |||
Db  1236  ------------------AGAAACTACTTTCTGAAGATCTTGAAGGACCTGTGG  1271

Qy   338  --------------LysGlyLysArgGlyHisSerSerValSerThrGluSerGluSer  353
              |||||||  :::
```

```
Db                                                    |||                |||||||:::
        21661    ----------------------------TGCCTTGGTGACTACCCCGAGGTCCTCCAGGAAATC  21696
                                                                         :::

Qy        202    TrpMetValPheGlnHisIleMetValGlyLeuIleLeuProGlyIleVal  221
                     ||:|||       :::||       :::||| :::||       :||:|
Db      21697    TGGCCCGTGCTCCCGCAATGTGGAAACAAATTTCTTGGCTTCCTACTCCCCGCTCATT  21756

Qy        222    IleLeuSerCysTyrCysIleIleIleSerLysHisSerLysGlyHisGlnLys  241
                     :::       |||||||       |||||||       ||||:::|||
Db      21757    ATGAGTTATTGCTACTTCAGAATCATCCAGACGCTGTTYTCCTGCAAGAACCACAAGAA  21816

Qy        242    ArgLysAlaLeuLysThrThrValIleLeuLeuIleLeuAlaCysTrpLeuPro  261
                     ||||:||       :::::::::       ||||||       ||       ||
Db      21817    GCCAAAGCCATTAAACTGATCCTTCTGGTGGTCATCGTGTTTTTCCTCTTCTGGACACCC  21876

Qy        262    TyrTyrValGlyIleSerIleAspSerPheIleLeuLeuGlyValIleLysGlnGlyCys  281
                     ||       :::::::::       |||       |||
Db      21877    TACAACRTTATGATTTTCCTGGAGACGCTTAAGCTCTATGACTTCTTT---CCCAGTTGT  21933

Qy        282    AspPheGluSerIleValHisLysTrpIleSerIleThrGluAlaLeuAlaPhePheHis  301
                     ||       :::||||||       :::||||||||||||       |||||||
Db      21934    GACATGAGGAAGGATCTGAGGCTGGCCCCTCAGTGTGACTGAGAGAYGGTTGCATTTAGCCAT  21993

Qy        302    CysCysLeuAsnProIleLeuTyrAlaPheLeuGlyAlaLysPheLysSerSerAlaGln  321
                     ||       ||||||||       |||||||       ||||||:::
Db      21994    TGTTGCCTGAATCCTCTCATCATGCATTTGCTGGGGAGAAGTTCAGAAGATACCTTTAC  22053

Qy        322    HisAlaLeuAsnSerMetSerArgGlySerLeuLysIleLeu------------  336
                     |||       :::|||       :::|||
Db      22054    CACCTGTAT--------------GGGAAATGCCTGGCTGTCCTGTCTGGGCGCCTCAGTC  22098

Qy        337    ------------SerLysGlyLysArgGlyGlyHisSerSerValSerThrGlu  350
                     ||:::       :::|||       :||:||
Db      22099    CACGTTGATTTCTCCTCATCTGAATCACAAAGGAGCAGGCATGGAAGTGTTCTG------  22152

Qy        351    SerGluSerSerPheHisSerSer  359
                     ||       :::||:::|||
Db      22153    AGCAGCAATTTTACTTACCACACGAGT  22179
```

Search completed: January 11, 2006, 02:49:02
Job time : 282 secs